

From: Myers, Carla  
Sent: Wednesday, October 05, 2005 4:35 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search 09/887941

Please do an oligomer search in commercial and interference files for fragments of SEQ ID NO: 1-10 -  
please limit the search results to  
nucleic acids of a length of 50 nucleotides or less.

please provide a printout of the first 40 results.

The CRF has been entered; [http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL\\_ID=09887941](http://expoweb1:8001/cgi-bin/expo/BioInfo/bioquery.pl?APPL_ID=09887941)

Thank you

Carla Myers  
AU 1634  
Reimsen Bldg / Rm 2E79  
Mailbox: REM 2C70  
571-272-0747

RECEIVED  
OCT -5 2005  
STIC/BIOTECH. DIVISION  
(STIC)

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIS: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 04:55:56 : Search time 330.119 Seconds  
(without alignments)  
4336.068 Million cell updates/sec

Title: US-09-887-941B-10

Perfect score: 215  
Sequence: 1 acgcgcgcacacgtctctca.....attctgtacgcgcgcgcgc 215

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 8443130 seqs, 3482420727 residues

Word size : 0

Total number of hits satisfying chosen parameters: 10399348

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database : Published Applications NA.\*

1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
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10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
14: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
15: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
16: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
17: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
18: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
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21: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
22: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
23: /cgn2\_6/ptodata/2/pubpna/US11\_PUBCOMB.seq:\*  
24: /cgn2\_6/ptodata/2/pubpna/US11\_PUBCOMB.seq:\*  
25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	8.4	25	22	US-10-719-956-430481
2	16	7.4	25	21	US-10-719-900-335376
3	16	7.4	25	21	US-10-719-900-379840
4	16	7.4	25	21	US-10-719-900-567937
5	16	7.4	25	24	US-11-036-317-139770
6	16	7.4	25	24	US-11-036-317-615245
7	16	7.4	25	24	US-11-036-317-615975

8	15	7.0	25	21	US-10-719-900-278239	Sequence 278239,
9	15	7.0	25	21	US-10-719-900-806136	Sequence 806136,
10	15	7.0	25	21	US-10-809-189-14636	Sequence 14636, A
11	15	7.0	25	21	US-10-809-189-14653	Sequence 14653, A
12	15	7.0	25	21	US-10-956-157-130791	Sequence 130791,
13	15	7.0	25	21	US-10-956-157-134955	Sequence 134955,
14	15	7.0	25	21	US-10-956-157-137770	Sequence 137770,
15	15	7.0	25	21	US-10-956-157-150085	Sequence 150085,
16	15	7.0	25	21	US-10-956-157-150649	Sequence 150649,
17	15	7.0	25	21	US-10-956-157-164027	Sequence 164027,
18	15	7.0	25	21	US-10-956-157-169794	Sequence 169794,
19	15	7.0	25	21	US-10-956-157-177304	Sequence 177304,
20	15	7.0	25	21	US-10-956-157-181926	Sequence 181926,
21	15	7.0	25	21	US-10-956-157-218881	Sequence 218881,
22	15	7.0	25	21	US-10-956-157-217475	Sequence 217475,
23	15	7.0	25	21	US-10-956-157-285224	Sequence 285224,
24	15	7.0	25	21	US-10-956-157-293960	Sequence 293960,
25	15	7.0	25	22	US-10-719-956-219909	Sequence 219909,
26	15	7.0	25	22	US-10-719-956-266795	Sequence 266795,
27	15	7.0	25	22	US-10-719-956-297916	Sequence 297916,
28	15	7.0	25	22	US-10-719-956-673483	Sequence 673483,
29	15	7.0	25	22	US-11-036-317-210546	Sequence 210546,
30	15	7.0	25	24	US-11-036-317-229485	Sequence 229485,
31	15	7.0	25	24	US-11-036-317-324494	Sequence 324494,
32	15	7.0	25	24	US-11-036-317-380084	Sequence 380084,
33	15	7.0	25	24	US-11-036-317-394974	Sequence 394974,
34	15	7.0	25	24	US-11-036-317-398301	Sequence 398301,
35	15	7.0	25	24	US-11-036-317-619585	Sequence 619585,
36	15	7.0	25	24	US-11-036-317-816552	Sequence 816552,
37	15	7.0	25	24	US-11-036-317-882725	Sequence 882725,
38	15	7.0	25	24	US-11-036-317-948953	Sequence 948953,
39	15	7.0	25	24	US-11-036-317-980463	Sequence 980463,
40	15	7.0	25	24	US-11-036-317-990609	Sequence 990609,
41	15	7.0	25	18	US-10-609-217-379	Sequence 379, App
42	15	7.0	45	18	US-10-632-388-379	Sequence 379, App
43	15	7.0	45	18	US-10-651-723-379	Sequence 379, App
44	15	7.0	45	18	US-10-645-761-379	Sequence 379, App
45	15	7.0	45	18	US-10-666-696-379	Sequence 379, App
46	15	7.0	45	18	US-10-653-048-379	Sequence 379, App
47	15	7.0	45	22	US-10-723-003-5	Sequence 5, Appl
48	15	7.0	50	17	US-10-645-784-379	Sequence 379, App
49	15	7.0	50	17	US-10-131-827-7176	Sequence 7176, Ap
50	15	7.0	25	19	US-10-098-2638-59411	Sequence 59411, A
51	14	6.5	25	19	US-10-719-900-448093	Sequence 448093,
52	14	6.5	25	21	US-10-719-900-486424	Sequence 486424,
53	14	6.5	25	21	US-10-719-900-499088	Sequence 499088,
54	14	6.5	25	21	US-10-719-900-530468	Sequence 530468,
55	14	6.5	25	21	US-10-719-900-679604	Sequence 679604,
56	14	6.5	25	21	US-10-719-900-688526	Sequence 688526,
57	14	6.5	25	21	US-10-719-900-776300	Sequence 776300,
58	14	6.5	25	21	US-10-719-900-824111	Sequence 824111,
59	14	6.5	25	21	US-10-719-900-900826	Sequence 900826,
60	14	6.5	25	21	US-10-719-900-911902	Sequence 911902,
61	14	6.5	25	21	US-10-719-900-914346	Sequence 914346,
62	14	6.5	25	21	US-10-809-189-88690	Sequence 88690, A
63	14	6.5	25	21	US-10-809-189-88691	Sequence 88691, A
64	14	6.5	25	21	US-10-956-157-142808	Sequence 142808,
65	14	6.5	25	21	US-10-956-157-172829	Sequence 172829,
66	14	6.5	25	21	US-10-956-157-172890	Sequence 172890,
67	14	6.5	25	21	US-10-956-157-216177	Sequence 216177,
68	14	6.5	25	21	US-10-956-157-221366	Sequence 221366,
69	14	6.5	25	21	US-10-956-157-248153	Sequence 248153,
70	14	6.5	25	21	US-10-956-157-255905	Sequence 255905,
71	14	6.5	25	21	US-10-956-157-267379	Sequence 267379,
72	14	6.5	25	21	US-10-956-157-281134	Sequence 281134,
73	14	6.5	25	21	US-10-956-157-295683	Sequence 295683,
74	14	6.5	25	21	US-10-956-157-304582	Sequence 304582,
75	14	6.5	25	21	US-10-499-717-44	Sequence 44, Appl
76	14	6.5	25	22	US-10-719-956-361	Sequence 361, App
77	14	6.5	25	22	US-10-719-956-43795	Sequence 43795, A
78	14	6.5	25	22	US-10-719-956-67100	Sequence 67100, A
79	14	6.5	25	22	US-10-719-956-67100	Sequence 67100, A
80	14	6.5	25	22	US-10-719-956-78398	Sequence 78398, A

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c 81 14 6.5 25 22 US-10-719-956-88069, A
82 14 6.5 25 22 US-10-719-956-471310,
83 14 6.5 25 22 US-10-719-956-471315,
84 14 6.5 25 22 US-10-719-956-426757,
85 14 6.5 25 22 US-10-719-956-471887,
86 14 6.5 25 22 US-11-036-317-34756,
87 14 6.5 25 24 US-11-036-317-126909,
88 14 6.5 25 24 US-11-036-317-145174,
89 14 6.5 25 24 US-11-036-317-180236,
90 14 6.5 25 24 US-11-036-317-197701,
91 14 6.5 25 24 US-11-036-317-256553,
92 14 6.5 25 24 US-11-036-317-290634,
93 14 6.5 25 24 US-11-036-317-290634,
94 14 6.5 25 24 US-11-036-317-321487,
95 14 6.5 25 24 US-11-036-317-411048,
96 14 6.5 25 24 US-11-036-317-473214,
97 14 6.5 25 24 US-11-036-317-483701,
98 14 6.5 25 24 US-11-036-317-665577,
99 14 6.5 25 24 US-11-036-317-666848,
100 14 6.5 25 24 US-11-036-317-700492,
Sequence 88069, A
Sequence 371310,
Sequence 417985,
Sequence 426757,
Sequence 471887,
Sequence 34756, A
Sequence 126909,
Sequence 145174,
Sequence 180236,
Sequence 197701,
Sequence 256553,
Sequence 290634,
Sequence 290634,
Sequence 321487,
Sequence 411048,
Sequence 473214,
Sequence 483701,
Sequence 665577,
Sequence 666848,
Sequence 700492,
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## ALIGNMENTS

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RESULT 1
US-10-719-956-430481
; Sequence 430481, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 430481
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-430481
```

```
Query Match 8.4%; Score 18; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 184 GTTGCTGTGTCATTGT 201
Db 4 GTTGCTGTGTCATTGT 21
```

```
RESULT 2
US-10-719-900-335376
```

```
; Sequence 335376, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 335376
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-335376
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Query Match 7.4%; Score 16; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 177 GAGTTTCGTGCTGTG 192
Db 7 GAGTTTCGTGCTGTG 22
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```
RESULT 3
US-10-719-900-379840/c
```

```
; Sequence 379840, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 379840
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-379840
```

```
Query Match 7.4%; Score 16; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 6 GGCACAGTCTTCAG 21
Db 16 GGCACAGTCTTCAG 1
```

```
RESULT 4
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US-10-719-900-567937/c
; Sequence 567937, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002 11 20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 567937
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-567937
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```
Query Match 7.4%; Score 16; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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OY 6 GGCACAGTCTTCAG 21
Db 19 GGCACAGTCTTCAG 4
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```
RESULT 5
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US-11-036-317-139770/c
; Sequence 139770, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:25:05 : Search time 65.9759 Seconds  
(without alignments)  
5332.244 Million cell updates/sec

Title: US-09-887-941B-10

Perfect score: 215  
Sequence: 1 acgcgcgcacagctctca.....atttgtgagcgcgcgcgc 215

Scoring table: OLIGO NUC  
Gapop 60.0, Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

Issued Patents NA:\*

- 1: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/prodata/1/ina/5A\_COMB.seq:\*
- 4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/prodata/1/ina/PCTUS\_COMB.seq:\*
- 6: /cgn2\_6/prodata/1/ina/backfile1.seq:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	7.0	25	4	US-09-396-196G-14636
2	15	7.0	25	4	US-09-396-196G-14653
3	15	7.0	25	4	US-09-428-082B-379
4	15	7.0	50	4	US-08-030-175-31
5	14	6.5	18	2	US-08-350-260A-564
6	14	6.5	18	4	US-09-104-337A-564
7	14	6.5	25	4	US-09-396-196G-98690
8	14	6.5	25	4	US-09-396-196G-98691
9	14	6.5	39	2	US-08-350-260A-582
10	14	6.5	39	4	US-09-104-337A-582
11	14	6.5	41	2	US-08-350-260A-579
12	14	6.5	41	2	US-08-350-260A-580
13	14	6.5	41	2	US-08-350-260A-581
14	14	6.5	41	2	US-08-350-260A-585
15	14	6.5	41	2	US-08-350-260A-586
16	14	6.5	41	2	US-08-350-260A-588
17	14	6.5	41	2	US-08-350-260A-589
18	14	6.5	41	4	US-09-104-337A-579
19	14	6.5	41	4	US-09-104-337A-580
20	14	6.5	41	4	US-09-104-337A-585
21	14	6.5	41	4	US-09-104-337A-586
22	14	6.5	41	4	US-09-104-337A-588
23	14	6.5	41	4	US-09-104-337A-589
24	14	6.5	41	4	US-08-350-260A-557
25	14	6.5	44	2	US-08-350-260A-558
26	14	6.5	44	2	US-08-350-260A-559
27	14	6.5	44	2	US-08-350-260A-559

28	14	6.5	44	2	US-08-350-260A-560	Sequence 560, App
29	14	6.5	44	2	US-08-350-260A-561	Sequence 561, App
30	14	6.5	44	2	US-08-350-260A-562	Sequence 562, App
31	14	6.5	44	2	US-08-350-260A-583	Sequence 583, App
32	14	6.5	44	2	US-08-350-260A-584	Sequence 584, App
33	14	6.5	44	2	US-08-350-260A-587	Sequence 587, App
34	14	6.5	44	2	US-09-104-337A-557	Sequence 557, App
35	14	6.5	44	4	US-09-104-337A-558	Sequence 558, App
36	14	6.5	44	4	US-09-104-337A-559	Sequence 559, App
37	14	6.5	44	4	US-09-104-337A-560	Sequence 560, App
38	14	6.5	44	4	US-09-104-337A-561	Sequence 561, App
39	14	6.5	44	4	US-09-104-337A-562	Sequence 562, App
40	14	6.5	44	4	US-09-104-337A-583	Sequence 583, App
41	14	6.5	44	4	US-09-104-337A-584	Sequence 584, App
42	14	6.5	44	4	US-09-104-337A-587	Sequence 587, App
43	13	6.0	17	3	US-09-096-731A-23	Sequence 23, App1
44	13	6.0	19	3	US-09-038-637-141	Sequence 141, App
45	13	6.0	19	3	US-09-262-773-24	Sequence 24, App1
46	13	6.0	19	3	US-09-262-773-25	Sequence 25, App1
47	13	6.0	21	4	US-09-856-072A-8	Sequence 8, App1
48	13	6.0	25	4	US-09-396-196G-14760	Sequence 14760, A
49	13	6.0	25	4	US-09-396-196G-70565	Sequence 70565, A
50	13	6.0	25	4	US-09-396-196G-70566	Sequence 70566, A
51	13	6.0	25	4	US-09-396-196G-113519	Sequence 113519, A
52	13	6.0	25	4	US-09-396-196G-113520	Sequence 113520, A
53	13	6.0	25	4	US-09-396-196G-113521	Sequence 113521, A
54	13	6.0	25	4	US-09-396-196G-118227	Sequence 118227, A
55	13	6.0	25	4	US-09-396-196G-118228	Sequence 118228, A
56	13	6.0	25	4	US-09-396-196G-118239	Sequence 118239, A
57	13	6.0	25	4	US-09-396-196G-118240	Sequence 118240, A
58	13	6.0	42	1	US-07-834-539A-14	Sequence 14, App1
59	13	6.0	42	1	US-08-053-131-22	Sequence 22, App1
60	13	6.0	42	1	US-08-645-641-22	Sequence 22, App1
61	13	6.0	42	1	US-07-853-408B-22	Sequence 22, App1
62	13	6.0	42	1	US-08-096-762-22	Sequence 22, App1
63	13	6.0	42	2	US-08-800-353-14	Sequence 14, App1
64	13	6.0	42	2	US-08-308-865-22	Sequence 22, App1
65	13	6.0	42	3	US-09-042-353-190	Sequence 190, App
66	13	6.0	42	3	US-08-758-417A-38	Sequence 38, App1
67	13	6.0	42	5	PCT-US92-06185-14	Sequence 14, App1
68	13	6.0	42	5	PCT-US92-10983-22	Sequence 22, App1
69	13	6.0	45	2	US-08-350-260A-545	Sequence 545, App
70	13	6.0	45	2	US-08-350-260A-546	Sequence 546, App
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78	12	5.6	15	1	US-08-398-305-17	Sequence 17, App1
79	12	5.6	15	1	US-08-705-225-17	Sequence 17, App1
80	12	5.6	15	4	US-09-641-690A-5	Sequence 5, App1
81	12	5.6	15	4	US-09-798-689-20	Sequence 20, App1
82	12	5.6	17	1	US-08-640-378-22	Sequence 22, App1
83	12	5.6	17	1	US-09-298-886-4	Sequence 4, App1
84	12	5.6	17	4	US-09-076-776-9	Sequence 9, App1
85	12	5.6	17	4	US-09-999-672-84	Sequence 4, App1
86	12	5.6	18	1	US-08-013-801-4	Sequence 4, App1
87	12	5.6	18	1	US-08-072-065-13	Sequence 13, App1
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94	12	5.6	18	3	US-08-885-366-13	Sequence 13, App1
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100	12	5.6	18	5	PCT-US95-03125-4	Sequence 4, App1



## ALIGNMENTS

## RESULT 1

US-09-396-196G-14636  
; Sequence 14636, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Miltmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14636  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-14636

Query Match 7.0%; Score 15; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 AACCTATAGCTGTCC 16

## RESULT 2

US-09-396-196G-14653  
; Sequence 14653, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Miltmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14653  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-14653

Query Match 7.0%; Score 15; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 AACCTATAGCTGTCC 69  
|||||  
Db 5 AACCTATAGCTGTCC 19

RESULT 3  
US-09-428-082B-379/c  
; Sequence 379, Application US/09428082B  
; Patent No. 6660843

## GENERAL INFORMATION:

APPLICANT: FEIGE, ULRICH  
APPLICANT: LIU, CHUAN-FA  
APPLICANT: CHESTNAM, JANET C.  
APPLICANT: BOONE, THOMAS CHARLES  
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS  
FILE REFERENCE: A-527  
CURRENT APPLICATION NUMBER: US/09/428,082B  
CURRENT FILING DATE: 1999-10-22  
PRIOR APPLICATION NUMBER: 60/105,371  
PRIOR FILING DATE: 1998-10-23  
NUMBER OF SEQ ID NOS: 1133  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 379  
LENGTH: 45  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: TMP-TMP-FC  
US-09-428-082B-379

Query Match 7.0%; Score 15; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 116 CACCGCTCCACGCG 130  
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Db 28 CACCGCTCCACGCG 14

## RESULT 4

US-08-030-175-31/c  
; Sequence 31, Application US/08030175  
; Patent No. 6767996  
; GENERAL INFORMATION:  
; APPLICANT: Gorman, Scott D.  
; APPLICANT: Clark, Michael R.  
; APPLICANT: Cobbold, Stephen P.  
; APPLICANT: Waldmann, Herman  
; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION  
; NUMBER OF SEQUENCES: 43  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Rothwell, Figsy, Ernst & Kurz, P. C.  
; STREET: 555 13TH ST., NW Suite 701 East  
; CITY: Washington  
; STATE: D. C.  
; COUNTRY: U.S.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk, 5.25 inch, 360 KB storage  
; COMPUTER: IBM AT compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2  
; SOFTWARE: WordPerfect 5.0 (Dos text)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/030,175  
; FILING DATE: 17-MAY-1993  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/GB91/01578  
; FILING DATE: 13-SEP-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ernst, Barbara G.  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1768-113  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)783-6040  
; TELEFAX: (202)783-6031  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 50 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:22:30 ; Search time 1495.43 Seconds  
(without alignments)  
5472.564 Million cell updates/sec

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Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database : EST:\*

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6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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6	6.0	46	8	A2304027	A2304027 IM0003F12
7	6.0	47	8	A2769488	A2769488 IM0570F15
8	6.0	47	8	A2477112	A2477112 IM0296L20
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10	6.0	47	8	A2595068	A2595068 SP1032 KR
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31	5.6	50	1	AU103071	AU103071 AU103071
32	5.6	50	1	AU104420	AU104420 AU104420
33	5.6	50	1	AU104421	AU104421 AU104421
34	5.6	50	1	AU106547	AU106547 AU106547
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45	5.1	23	8	TA88A08P	TA88A08P T. brucei
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47	5.1	26	8	AG203256	AG203256 Pan. trogl
48	5.1	26	8	AZ789510	AZ789510 Pan. trogl
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50	5.1	29	8	AJ655586	AJ655586 AJ655586
51	5.1	30	1	AZ328130	AZ328130 IM0051D16
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100 11 5.1 47 8 AZ587600 AZ587600 1M0395F23

## ALIGNMENTS

## RESULT 1

BE373472 43 bp mRNA linear EST 21-JUL-2000  
LOCUS 601225842F1 NCI\_CGAP\_Mam1 Mus musculus cDNA clone IMAGE:3584194 5',  
DEFINITION mRNA sequence.

ACCESSION BE373472  
VERSION BE373472.1 GI:9318835

KEYWORDS EST.  
SOURCE Mus musculus (house mouse)

## ORGANISM

## REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov

## COMMENT

Tissue Procurement: Gilbert Smith, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LIML at:  
http://image.liml.gov  
Plate: LAM8742 row: c column: 11  
High quality sequence stop: 43.  
Location/Qualifiers  
1. 43

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/note="Organ: mammary; Vector: pCMV-SPORT6; Site\_1: SalI;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dT.  
Library constructed by Life Technologies. Investigator  
providing samples: Gilbert Smith, NIH"

## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1.7e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 GACCTCCACACGG 151  
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Db 9 GACCTCCACACGG 22

## RESULT 2

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LOCUS AUI06554 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone  
DEFINITION KAT05773, mRNA sequence.

ACCESSION AUI06554  
VERSION AUI06554.1 GI:13556075

KEYWORDS EST.  
SOURCE Homo sapiens (human)

## ORGANISM

Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

## REFERENCE

1 (bases 1 to 50)

## AUTHORS

Suzuki, Y., Taira, H., Tsunoda, T., Mizushima-Sugano, J., Sese, J.,  
Hata, H., Ota, T., Isogai, T., Tanaka, T., Morishita, S., Okubo, K.,  
Sakaki, Y., Nakamura, Y., Suyama, A., and Sugano, S.  
Diverse transcriptional initiation revealed by fine, large-scale  
mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

## TITLE

## JOURNAL

## MEDLINE

## PUBMED

11375929

## COMMENT

Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuk@iims.u-tokyo.ac.jp  
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A., and  
Sugano, S. Construction and characterization of a full  
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),  
149-156 (1997).

## FEATURES

source

/organism="Homo sapiens"  
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## ORIGIN

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GCCGGCCACAGTTC 16  
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Db 12 GCCGGCCACAGTTC 25

## RESULT 3

AZ841487 30 bp DNA linear GSS 20-FEB-2001  
LOCUS AZ841487/c 2M0139C01R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
DEFINITION clone UGCGM0139C01 R, genomic survey sequence.

ACCESSION AZ841487

AZ841487.1 GI:13011395

## VERSION

GSS.

## KEYWORDS

Mus musculus (house mouse)

## SOURCE

Mus musculus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A., and Wright, D. Weiss, R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

## AUTHORS

Contact: Robert B. Weiss

## JOURNAL

University of Utah

## COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0139 row: C column: 01  
Seq primer: CACACAGAAACAGCTATGACC  
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High quality sequence stop: 30.  
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1. 30  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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10: Geneseq2003cs:\*  
11: Geneseq2003ds:\*  
12: Geneseq2004as:\*  
13: Geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15	7.0	45	3	AA69465 Synthetic
C 2	15	7.0	45	6	ABL35708 TWP-TWP g
C 3	15	7.0	50	6	ABZ07185 Human leu
4	14	6.5	17	10	ADD20923 Human GAP
5	14	6.5	17	10	ADD20926 Human GAP
6	14	6.5	17	10	ADD20924 Human GAP
7	14	6.5	17	10	ADD20925 Human GAP
8	14	6.5	25	9	ACT159420 Human mic
C 9	10	6.5	25	10	ADD01408 Human TCH
10	14	6.5	25	10	ADD21221 Human GAP
11	14	6.5	25	10	ADD21215 Human GAP
12	14	6.5	25	10	ADD21216 Human GAP
13	14	6.5	25	10	ADD21222 Human GAP
14	14	6.5	25	10	ADD21211 Human GAP
15	14	6.5	25	10	ADD21220 Human GAP
16	14	6.5	25	10	ADD21212 Human GAP
17	14	6.5	25	10	ADD21214 Human GAP
18	14	6.5	25	10	ADD21219 Human GAP
19	14	6.5	25	10	ADD21218 Human GAP
20	14	6.5	25	10	ADD21217 Human GAP

21	14	6.5	25	10	ADD21213	ADD21213 Human GAP
C 22	14	6.5	25	12	ADP17305	ADP17305 Renal cel
23	14	6.5	39	5	AA683903	AA683903 PCR prime
24	14	6.5	41	5	AA683902	AA683902 PCR prime
25	14	6.5	41	5	AA683906	AA683906 PCR prime
26	14	6.5	41	5	AA683901	AA683901 PCR prime
27	14	6.5	41	5	AA683900	AA683900 PCR prime
28	14	6.5	41	5	AA683907	AA683907 PCR prime
29	14	6.5	41	5	AA683910	AA683910 PCR prime
30	14	6.5	41	5	AA683909	AA683909 PCR prime
31	14	6.5	44	4	AA683935	AA683935 Human PH1
32	14	6.5	44	5	AA683896	AA683896 PCR prime
33	14	6.5	44	5	AA683904	AA683904 PCR prime
34	14	6.5	44	5	AA683895	AA683895 PCR prime
35	14	6.5	44	5	AA683894	AA683894 PCR prime
36	14	6.5	44	5	AA683895	AA683895 PCR prime
37	14	6.5	44	5	AA683908	AA683908 PCR prime
38	14	6.5	44	5	AA683897	AA683897 PCR prime
39	14	6.5	44	5	AA683898	AA683898 PCR prime
40	14	6.5	44	5	AA683899	AA683899 PCR prime
41	14	6.5	44	10	ABX79090	ABX79090 Mucin 1 (
42	14	6.5	48	6	ABK24115	ABK24115 laminin p
C 43	14	6.5	50	4	AA176799	AA176799 Human sll
C 44	13	6.0	15	6	ABL45847	ABL45847 Human EDG
45	13	6.0	17	2	AAV96402	AAV96402 Potato ci
46	13	6.0	17	2	AAV96403	AAV96403 Potato ci
C 47	13	6.0	17	2	AAV99312	AAV99312 C. elegans
48	13	6.0	17	10	ADB40744	ADB40744 Tumour su
49	13	6.0	17	10	ADD20922	ADD20922 Human GAP
50	13	6.0	17	10	ADD20927	ADD20927 Human GAP
C 51	13	6.0	18	2	AAZ21791	AAZ21791 Exemplary
C 52	13	6.0	18	6	ABT05110	ABT05110 TNFRI exp
C 53	13	6.0	18	13	ADP06140	ADP06140 Human TNF
C 54	13	6.0	19	2	AAQ92486	AAQ92486 Cyclohexal
55	13	6.0	19	2	AAZ26850	AAZ26850 Human chr
56	13	6.0	19	2	AAZ26849	AAZ26849 Human chr
57	13	6.0	19	10	ADG34897	ADG34897 Human TNF
C 58	13	6.0	19	10	ADG35020	ADG35020 Human TNF
59	13	6.0	20	2	AAV09923	AAV09923 Fusarium
60	13	6.0	20	12	ADH68616	ADH68616 Rosa sp f
C 61	13	6.0	21	4	AAF82345	AAF82345 MYRINE IN
C 62	13	6.0	21	6	ABO81614	ABO81614 INOS rela
C 63	13	6.0	21	10	ACF79346	ACF79346 Phenylala
64	13	6.0	21	12	ADK95295	ADK95295 Primer of
C 65	13	6.0	23	12	ADN35332	ADN35332 Human NSC
C 66	13	6.0	23	12	ADN48538	ADN48538 PCR prime
C 67	13	6.0	24	3	ABK10968	ABK10968 PCR prime
68	13	6.0	24	6	AB182804	AB182804 Capture o
69	13	6.0	24	6	AB192071	AB192071 Capture o
C 70	13	6.0	24	6	AB192071	AB192071 Capture o
C 71	13	6.0	24	6	AB182805	AB182805 Capture o
C 72	13	6.0	25	6	ABK66313	ABK66313 Mouse TGR
73	13	6.0	25	9	ACH59338	ACH59338 DNA target
74	13	6.0	25	10	ADD21223	ADD21223 Human GAP
75	13	6.0	25	10	ADD21210	ADD21210 Human GAP
C 76	13	6.0	29	10	ADK71528	ADK71528 Drug-tole
C 77	13	6.0	31	6	ABK21680	ABK21680 Human ERG
C 78	13	6.0	31	8	ABZ64249	ABZ64249 Human H-R
C 79	13	6.0	31	8	ABZ66128	ABZ66128 Human HER
C 80	13	6.0	31	8	ACD61854	ACD61854 HCV minus
C 81	13	6.0	31	12	AD190049	AD190049 HCV DNAzy
C 82	13	6.0	33	6	ABA04974	ABA04974 Ribosomal
83	13	6.0	35	10	ADL07530	ADL07530 F. pastor
84	13	6.0	39	10	ABZ26067	ABZ26067 EHV BAC r
85	13	6.0	39	12	ADH70031	ADH70031 Human Vbe
C 86	13	6.0	39	12	ADL64622	ADL64622 Human Vbe
C 87	13	6.0	39	12	ADQ36116	ADQ36116 Human Vbe
C 88	13	6.0	40	3	AAA51111	AAA51111 Exophiala
89	13	6.0	40	3	AAA51142	AAA51142 Oligomer
90	13	6.0	40	6	ABK69697	ABK69697 Human WTL
91	13	6.0	40	8	ACA93699	ACA93699 Recombina
92	13	6.0	40	10	ADB67573	ADB67573 Human WT-
93	13	6.0	40	10	ADJ80806	ADJ80806 Wilms' s tu

94	13	6.0	40	12	ADJ83726	Oligonucle
95	13	6.0	40	12	ADJ57614	Human WT-
96	13	6.0	40	12	ADJ09169	Human WT1
97	13	6.0	42	2	AAQ23424	Probe for
98	13	6.0	42	2	AAQ44162	Probe to
99	13	6.0	42	2	AAJ37218	inse
100	13	6.0	42	2	AAV12516	Probe for

## ALIGNMENTS

## RESULT 1

AAA69465/C  
ID AAA69465 standard; DNA; 45 BP.

AAA69465;

31-OCT-2000 (first entry)

Synthetic TMP-Fc gene construction oligonucleotide SEQ ID NO:379.

Modified peptide; therapeutic agent; fusion; Fc domain; cancer;  
autoimmune disease; cytostatic; antineoplastic; thrombolytic; VEGF;  
immunosuppressive; EPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP;  
inhibitor; erythropoietin; thrombopoietin; interleukin 1;  
cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;  
vascular endothelial growth factor; matrix metalloproteinase; asthma;  
thrombosis; pharmaceutical; PCR primer; ss.

Homo sapiens.  
Synthetic.

WO200024782-A2.

04-MAY-2000.

25-OCT-1999; 99WO-US025044.

23-OCT-1998; 98US-0105371P.

22-OCT-1999; 99US-00428082.

(AMGE-) AMGEN INC.

Feige U, Liu C, Cheetham J, Boone TC;

WPI; 2000-350702/30.

Novel composition of matter comprising an Fc domain and pharmacologically  
active peptides, useful for treating cancer and autoimmune diseases.

Example 2; Page 329; 608pp; English.

The present invention describes composition of matter (I) comprising an  
Fc domain, pharmacologically active peptides, and linkers. Where (I) is:  
(X1)-a-P1-(X2)b, where: P1 = an Fc domain; X1 and X2 = are each  
independently selected from -(L1)-C-P1, -(L1)-C-P1-(L2)-d-P2, -(L1)-C-P1-  
(L2)-d-P2-(L3)-e-P3, or -(L1)-C-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,  
P3, and P4 = are each independently sequences of pharmacologically active  
peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,  
c, d, e, and f = are each independently 0 or 1, provided that at least 1  
of a and b is 1. The composition can have cytostatic, antineoplastic,  
thrombolytic and immunosuppressive activities. DNAs, vectors and host  
cells from the present invention can be used for producing pharmaceutical  
compositions. The compositions are useful for treating cancer, asthma,  
thrombosis, or autoimmune diseases. The use of an Fc domain (rather than  
a Fab domain) can provide a longer half-life or incorporate functions  
such as Fc receptor binding, protein A binding, complement fixation, and  
possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to  
AAB18003 represent nucleotide and amino acid sequences used in the  
exemplification of the present invention

Sequence 45 BP; 9 A; 11 C; 17 G; 8 T; 0 U; 0 Other;

Query Match	7.0%	Score 15;	DB 3;	Length 45;
Best Local Similarity	100.0%	Pred. No. 8.2e+02;		
Matches 15;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
116	CACCGCCTCCACACAG	130		
116				
28	CACCGCCTCCACACAG	14		

## RESULT 2

ABL35708/C  
ID ABL35708 standard; DNA; 45 BP.

ABL35708;

05-APR-2002 (first entry)

TMF-TMP gene construction oligonucleotide SEQ ID NO:379.

Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;  
erythropoietin; TPO; tumour necrosis factor alpha inhibitor;  
TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TMF;  
TPO mimetic peptide; EPO mimetic peptide; EGF; VEGF antagonist;  
MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;  
cytostatic; antineoplastic; antiarthritic; antidiabetic; ophthalmological;  
antineoplastic; anorectic; antiferility; haemostatic; dermatological;  
neuroprotective; inflammatory disease; autoimmune disease; tumour growth;  
cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;  
sleep disorder; neurological degenerative disease; anaemia;  
thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;  
Fanconi's syndrome; PCR primer; ss.

Homo sapiens.  
Synthetic.

WO200183525-A2.

08-NOV-2001.

02-MAY-2001; 2001WO-US014310.

03-MAY-2000; 2000US-00563286.

(AMGE-) AMGEN INC.

Feige U, Liu C, Cheetham JC, Boone TC, Gudas JW;

WPI; 2002-130313/17.

Novel vehicle-peptide molecule or its multimers useful for treating  
inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,  
diabetic retinopathy, obesity, sleep disorders and infertility.

Example 2; Page 103; 176pp; English.

The present invention describes a vehicle-peptide molecule (I) or its  
multimers. (I) can have antineoplastic, antitumour, immunosuppressive,  
cytostatic, antineoplastic, antiarthritic, antidiabetic, ophthalmological,  
antineoplastic, anorectic, antiferility, haemostatic, dermatological and  
neuroprotective activities. (I) can be used as a therapeutic or  
prophylactic agent as well as for screening purposes. (I) is useful for  
diagnosing diseases characterised by dysfunction of their associated  
protein of interest, for identifying normal or abnormal proteins of  
interest, as a part of diagnostic kit to detect the presence of their  
protein of interest in a biological sample. Additionally, (I) is useful  
for treating inflammatory and autoimmune diseases, tumour growth, cancer,  
rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders, EPO-  
infertility, and neurological degenerative diseases. (I), comprising EPO-  
mimetic compounds are useful for treating disorders characterised by low  
red blood cell levels such as anaemia. The TPO-mimetic comprising  
compounds are useful for treating conditions that involve an existing  
megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet

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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 04:55:56 ; Search time 222.638 Seconds  
(without alignments)  
4536.068 Million cell updates/sec

Title: US-09-887-941B-9

Perfect score: 145  
Sequence: 1 tggagagcagcattccctccct.....mnaagttgagctctcc 145

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 844130 seqs, 3482420727 residues

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Minimum DB seq length: 0  
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Post-processing: Listing first 100 summaries

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26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	11.7	25	21	US-10-719-900-170745
2	17	11.7	25	21	US-10-809-189-5883
3	17	11.7	25	22	US-10-719-956-524224
4	16	11.0	25	21	US-10-809-189-122026
5	16	11.0	25	21	US-10-956-157-201846
6	16	11.0	25	21	US-10-956-157-247188
7	16	11.0	25	21	US-10-956-157-253662

8	16	11.0	25	24	US-11-036-317-94502	Sequence 94502, A
9	16	11.0	25	24	US-11-036-317-95477	Sequence 95477, A
10	15	10.3	17	10	US-09-848-754A-445	Sequence 445, App
11	15	10.3	17	10	US-09-848-754A-1750	Sequence 1750, App
12	15	10.3	22	22	US-10-845-057-143	Sequence 143, App
13	15	10.3	22	22	US-10-845-057-449	Sequence 449, App
14	15	10.3	25	21	US-10-719-900-108447	Sequence 108447, A
15	15	10.3	25	21	US-10-719-900-409239	Sequence 409239, A
16	15	10.3	25	21	US-10-809-189-38929	Sequence 38929, A
17	15	10.3	25	21	US-10-956-157-304970	Sequence 304970, A
18	15	10.3	25	22	US-10-719-956-3771	Sequence 3771, App
19	15	10.3	24	24	US-11-036-317-567671	Sequence 567671, A
20	15	10.3	17	10	US-09-848-754A-1749	Sequence 1749, App
21	14	9.7	17	21	US-10-363-177A-46	Sequence 43, App1
22	14	9.7	19	16	US-10-251-117-766	Sequence 766, App
23	14	9.7	19	16	US-10-251-117-1073	Sequence 1073, App
24	14	9.7	19	22	US-10-923-354-712	Sequence 712, App
25	14	9.7	19	22	US-10-923-354-1019	Sequence 1019, App
26	14	9.7	21	20	US-10-751-736-29063	Sequence 29063, A
27	14	9.7	21	20	US-10-751-736-32216	Sequence 32216, A
28	14	9.7	25	15	US-10-098-263B-84817	Sequence 84817, A
29	14	9.7	25	21	US-10-719-900-185005	Sequence 185005, A
30	14	9.7	25	21	US-10-719-900-246219	Sequence 246219, A
31	14	9.7	25	21	US-10-719-900-249184	Sequence 249184, A
32	14	9.7	25	21	US-10-719-900-260808	Sequence 260808, A
33	14	9.7	25	21	US-10-719-900-327252	Sequence 327252, A
34	14	9.7	25	21	US-10-719-900-335121	Sequence 335121, A
35	14	9.7	25	21	US-10-719-900-354142	Sequence 354142, A
36	14	9.7	25	21	US-10-719-900-534440	Sequence 534440, A
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38	14	9.7	25	21	US-10-719-900-642806	Sequence 642806, A
39	14	9.7	25	21	US-10-719-900-798504	Sequence 798504, A
40	14	9.7	25	21	US-10-719-900-824514	Sequence 824514, A
41	14	9.7	25	21	US-10-719-900-973647	Sequence 973647, A
42	14	9.7	25	21	US-10-809-189-7934	Sequence 7934, App
43	14	9.7	25	21	US-10-809-189-7945	Sequence 7945, App
44	14	9.7	25	21	US-10-809-189-7946	Sequence 7946, App
45	14	9.7	25	21	US-10-809-189-7947	Sequence 7947, App
46	14	9.7	25	21	US-10-956-157-84715	Sequence 84715, A
47	14	9.7	25	21	US-10-956-157-84716	Sequence 84716, A
48	14	9.7	25	21	US-10-956-157-84717	Sequence 84717, A
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51	14	9.7	25	21	US-10-956-157-179820	Sequence 179820, A
52	14	9.7	25	21	US-10-956-157-217933	Sequence 217933, A
53	14	9.7	25	21	US-10-956-157-222472	Sequence 222472, A
54	14	9.7	25	21	US-10-956-157-30813	Sequence 30813, A
55	14	9.7	25	22	US-10-719-956-30813	Sequence 30813, A
56	14	9.7	25	22	US-10-719-956-139856	Sequence 139856, A
57	14	9.7	25	22	US-10-719-956-307962	Sequence 307962, A
58	14	9.7	25	22	US-10-719-956-307962	Sequence 307962, A
59	14	9.7	25	24	US-11-036-317-77061	Sequence 77061, A
60	14	9.7	25	24	US-11-036-317-246886	Sequence 246886, A
61	14	9.7	25	24	US-11-036-317-346279	Sequence 346279, A
62	14	9.7	25	24	US-11-036-317-361234	Sequence 361234, A
63	14	9.7	25	24	US-11-036-317-387234	Sequence 387234, A
64	14	9.7	25	24	US-11-036-317-390960	Sequence 390960, A
65	14	9.7	25	24	US-11-036-317-397201	Sequence 397201, A
66	14	9.7	25	24	US-11-036-317-622381	Sequence 622381, A
67	14	9.7	25	24	US-11-036-317-903363	Sequence 903363, A
68	14	9.7	25	24	US-11-036-317-984504	Sequence 984504, A
69	14	9.7	25	24	US-11-036-317-986553	Sequence 986553, A
70	14	9.7	25	24	US-11-036-317-989882	Sequence 989882, A
71	14	9.7	46	14	US-10-112-488-48	Sequence 48, App1
72	13	9.0	13	20	US-10-257-017B-75567	Sequence 75567, A
73	13	9.0	13	20	US-10-257-017B-75568	Sequence 75568, A
74	13	9.0	19	10	US-09-848-754A-1748	Sequence 1748, App
75	13	9.0	17	9	US-09-860-784-52	Sequence 52, App1
76	13	9.0	20	9	US-09-263-959-1046	Sequence 1046, App
77	13	9.0	20	9	US-09-860-784-51	Sequence 51, App1
78	13	9.0	20	9	US-09-860-784-105	Sequence 105, App
79	13	9.0	21	9	US-09-860-784-49	Sequence 49, App1
80	13	9.0	22	9	US-09-860-784-49	Sequence 49, App1

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C 81 13 9.0 22 17 US-10-147-601A-5 Sequence 5, Appli
C 82 13 9.0 23 9 US-09-860-784-104 Sequence 104, App
C 83 13 9.0 25 15 US-10-098-263B-5398 Sequence 5398, Ap
C 84 13 9.0 25 15 US-10-098-263B-50326 Sequence 90326, A
C 85 13 9.0 25 21 US-10-719-900-7096 Sequence 7096, Ap
C 86 13 9.0 25 21 US-10-719-900-35838 Sequence 35838, A
C 87 13 9.0 25 21 US-10-719-900-59789 Sequence 59789, A
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C 91 13 9.0 25 21 US-10-719-900-113381 Sequence 113381,
C 92 13 9.0 25 21 US-10-719-900-171200 Sequence 171200,
C 93 13 9.0 25 21 US-10-719-900-178551 Sequence 178551,
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C 95 13 9.0 25 21 US-10-719-900-268928 Sequence 268928,
C 96 13 9.0 25 21 US-10-719-900-292775 Sequence 292775,
C 97 13 9.0 25 21 US-10-719-900-310642 Sequence 310642,
C 98 13 9.0 25 21 US-10-719-900-334579 Sequence 334579,
C 99 13 9.0 25 21 US-10-719-900-444765 Sequence 444765,
C 100 13 9.0 25 21 US-10-719-900-505181 Sequence 505181,
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## ALIGNMENTS

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RESULT 1
US-10-719-900-170745
; Sequence 170745, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 170745
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-719-900-170745
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Best Local Similarity 100.0%; Pred. No. 58;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 84 CCAAAATTCAGCTC 100
Db 3 CCAAAATTCAGCTC 19
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RESULT 2
US-10-809-189-5883
; Sequence 5883, Application US/10809189
; Publication No. US2005004851A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 5883
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-809-189-5883
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Query Match 11.7%; Score 17; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 84 CCAAAATTCAGCTC 100
Db 6 CCAAAATTCAGCTC 22
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```
RESULT 3
US-10-719-956-524224
; Sequence 524224, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT APPLICATION NUMBER: US/10/719,956
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,836
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 524224
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; US-10-719-956-524224
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Query Match 11.7%; Score 17; DB 22; Length 25;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 84 CCAAAATTCAGCTC 100
Db 7 CCAAAATTCAGCTC 23
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```
RESULT 4
US-10-809-189-122026
; Sequence 122026, Application US/10809189
; Publication No. US20050048531A1
; GENERAL INFORMATION:
; APPLICANT: Michael Miltmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/10/809,189
; CURRENT FILING DATE: 2004-03-25
; PRIOR APPLICATION NUMBER: US/09/396,196
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 122026
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-10-809-189-122026
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Query Match 11.0%; Score 16; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2,1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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## ALIGNMENTS

RESULT 1  
US-09-396-196G-5883

; Sequence 5883, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Miltmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affimetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 5883

; LENGTH: 25

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-396-196G-5883

Query Match 11.7%; Score 17; DB 4; Length 25;

Best Local Similarity 100.0%; Pred. No. 17;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 CCAAAATTCAGCTC 100

DB 6 CCAAAATTCAGCTC 22

RESULT 2  
US-09-238-972-12/C

; Sequence 12, Application US/09238972

; Patent No. 6784163

; GENERAL INFORMATION:

; APPLICANT: MacLeod, Carol L.

; TITLE OF INVENTION: Inhibition of Cationic Amino Acid Transporter Protein

; TITLE OF INVENTION: and Uses Thereof

; FILE REFERENCE: D5232CTP3

; CURRENT APPLICATION NUMBER: US/09/238,972

; CURRENT FILING DATE: 1999-01-27

; EARLIER APPLICATION NUMBER: US 08/187,634

; EARLIER FILING DATE: 1994-26-01

; NUMBER OF SEQ ID NOS: 16

; SEQ ID NO 12

; LENGTH: 25

; TYPE: DNA

; ORGANISM: artificial sequence

; FEATURE:

; NAME/KEY: primer bind

; OTHER INFORMATION: Primer used to clone the NOS2 cDNA by RT/PCR

; OTHER INFORMATION: from mouse mammary tumor cDNA

US-09-238-972-12

Query Match 11.0%; Score 16; DB 4; Length 25;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 92 TTCGAGCTCAAGACC 107

DB 25 TTCGAGCTCAAGACC 10

RESULT 3

US-09-396-196G-122026

; Sequence 122026, Application US/09396196G

; Patent No. 6821724

; GENERAL INFORMATION:

; APPLICANT: Michael Miltmann

; APPLICANT: David Mack

; APPLICANT: David Lockhart

; APPLICANT: Affimetrix, Inc.

; TITLE OF INVENTION: Methods of Genetic Analysis

; FILE REFERENCE: 3101.1

; CURRENT APPLICATION NUMBER: US/09/396,196G

; CURRENT FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/100,678

; PRIOR FILING DATE: 1998-09-17

; NUMBER OF SEQ ID NOS: 127806

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 122026

; LENGTH: 25

; TYPE: DNA

; ORGANISM: mus musculus

US-09-396-196G-122026

Query Match 11.0%; Score 16; DB 4; Length 25;

Best Local Similarity 100.0%; Pred. No. 60;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 92 TTCGAGCTCAAGACC 107

DB 4 TTCGAGCTCAAGACC 19

RESULT 4  
US-08-985-162-445

; Sequence 445, Application US/08985162

; Patent No. 6057156

; GENERAL INFORMATION:

; APPLICANT: Akhtar, Saghir

; APPLICANT: McSwigen, James

; TITLE OF INVENTION: ENZYMAIC NUCLEIC ACID TREATMENT

; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED

; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH

; TITLE OF INVENTION: FACTOR RECEPTORS

; NUMBER OF SEQUENCES: 1877

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lyon &amp; Lyon

; STREET: 633 West Fifth Street

; STREET: Suite 4700

; CITY: Los Angeles

; STATE: California

; COUNTRY: U.S.A.

; ZIP: 90071-2066

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

; MEDIUM TYPE: storage

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: IBM P.C. DOS 5.0

; SOFTWARE: FastSeq for Windows 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/985,162

; FILING DATE: 04 December 1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/036,476

; FILING DATE: 31 January 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Marburg, Richard J.

; REGISTRATION NUMBER: 32,327

; REFERENCE/DOCKET NUMBER: 230/107

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (213) 489-1600

; TELEFAX: (213) 955-0440

; TELEX: 67-3510

; INFORMATION FOR SEQ ID NO: 445:

; SEQUENCE CHARACTERISTICS:

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:22:30 ; Search time 1008.54 Seconds  
(without alignments)  
5472.564 Million cell updates/sec

Title: US-09-887-941B-9

Perfect score: 145  
Sequence: 1 tGagagcagcatcctccct.....mnaagttcagctctccc 145

Scoring table: OLIGO\_NTIC  
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

EST: \*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16	11.0	44	4	BG720096 602691016
C 2	15	10.3	39	8	AZ479867 1M0100H24
C 3	14	9.7	30	9	TA21H040
C 4	14	9.7	35	8	AZ345589 1M0080N16
C 5	14	9.7	37	1	AI1379566
C 6	13	9.0	21	2	AW246843 2822334.3
C 7	13	9.0	24	9	CM020455 GC0720 TT
C 8	13	9.0	31	1	AI439944 cl63d05.x
C 9	13	9.0	31	1	AU243401
C 10	13	9.0	34	1	AL934938
C 11	13	9.0	37	1	AI499210
C 12	13	9.0	37	4	BM399428 5009-0-57
C 13	13	9.0	38	8	AZ758198 1M0550P03
C 14	13	9.0	40	1	AA873888 cl05b07.s
C 15	13	9.0	41	7	D20673 HUMGS01649
C 16	13	9.0	46	1	AI619428 ty38a03.x
C 17	13	9.0	48	1	AU682688
C 18	13	9.0	50	9	CR207715 Forward s
C 19	13	8.3	28	1	AI376644 te63b01.x
C 20	12	8.3	31	1	AI537012
C 21	12	8.3	31	9	TA252803Q
C 22	12	8.3	32	8	BZ545461
C 23	12	8.3	32	8	CC057456
C 24	12	8.3	35	8	AZ806105 2M0067N21

C 25	12	8.3	37	4	BM396242
C 26	12	8.3	37	4	BM396513
C 27	12	8.3	38	8	BH903687
C 28	12	8.3	39	2	AV959991
C 29	12	8.3	39	8	AZ810683
C 30	12	8.3	40	1	AI123696
C 31	12	8.3	41	8	BH626532
C 32	12	8.3	41	9	CM020439
C 33	12	8.3	42	8	BH624960
C 34	12	8.3	43	1	AA878752
C 35	12	8.3	43	1	AI421857
C 36	12	8.3	43	4	AI814142
C 37	12	8.3	43	4	BI462985
C 38	12	8.3	43	8	AZ835722
C 39	12	8.3	44	1	AU663161
C 40	12	8.3	44	9	CL528502
C 41	12	8.3	46	1	AI355529
C 42	12	8.3	46	1	AI471447
C 43	12	8.3	46	1	AI680083
C 44	12	8.3	46	1	AI687405
C 45	12	8.3	47	9	CC795395
C 46	12	8.3	49	5	BQ417691
C 47	12	8.3	50	1	AV832923
C 48	12	8.3	50	4	BJ049388
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C 54	11	7.6	19	8	AZ474038
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C 57	11	7.6	20	8	AZ479839
C 58	11	7.6	20	8	AZ489864
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C 61	11	7.6	20	8	AZ809952
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C 67	11	7.6	21	8	AZ310220
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C 83	11	7.6	22	9	TA240H09P
C 84	11	7.6	23	8	AZ321671
C 85	11	7.6	23	9	TA157B05P
C 86	11	7.6	23	9	TA356B09P
C 87	11	7.6	24	1	AJ668296
C 88	11	7.6	24	5	EX563569
C 89	11	7.6	24	7	CF335916
C 90	11	7.6	24	8	AZ469660
C 91	11	7.6	24	8	AZ795776
C 92	11	7.6	25	1	AI149305
C 93	11	7.6	25	1	AI471126
C 94	11	7.6	25	1	AI471696
C 95	11	7.6	25	1	AI587718
C 96	11	7.6	25	1	AU256661
C 97	11	7.6	25	8	AZ664439

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BH903687	SALK_1031
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BH624960	1007091C0
AA878752	0F85d03.x
AI421857	LF55611.x
AI814142	WK63410.x
BI462985	603204504
AZ835722	2M0130C18
AJ663161	AA663161
CL528502	ASV17E02.
AI355529	qT76605.x
AI471447	tm11f04.x
AI680083	tw64h03.x
AI687405	td95f08.x
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AZ579566	1M0367L08
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AZ479839	1M0298C20
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AZ785856	2M0030M03
AZ809952	2M0074007
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AJ596416	Arabidops
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AZ476017	1M0294C02
AZ645640	1M0511N07
AZ663501	2M0232M07
AI275970	qW06G07.x
AI634352	ts59b12.x
AM247820	2820485.3
CF322673	HDN--01-L
CF326312	JMT1--05-
AZ310057	1M0018A15
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AZ598320	1M0413N04
AZ804465	2M0065Y09
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TA211D06P	T. brucei
TA240H09P	T. brucei
AZ321671	T. brucei
TA157B05P	T. brucei
TA356B09P	T. brucei
AJ668296	T. brucei
EX563569	BM396242
CF335916	JMT--05-M
AZ469660	1M0283J13
AZ795776	2M0051K11
AI149305	GC27d06.x
AI471126	tf90e05.x
AI471696	tf99f05.x
AI587718	AL587718
AU256661	AU256661
AZ664439	1M0544A07

98 11 7.6 25 8 AZ804762  
 C 99 11 7.6 25 8 AZ830405  
 C 100 11 7.6 25 8 AZ855418

AZ804762 2M0065N12  
 AZ830405 2M0109F12  
 AZ855418 2M0159M21

## ALIGNMENTS

RESULT 1  
 BG720096/c 44 bp mRNA linear EST 08-MAY-2001

DEFINITION 602691016F1 NIH\_MGC\_97 Homo sapiens CDNA clone IMAGE:4823642 5',  
 mRNA sequence.

ACCESSION BG720096  
 VERSION BG720096.1 GI:13999283  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE NIH-MGC Http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.

TISSUE Procurement: Miklos Palkovits, M.D., Ph.D.  
 CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki  
 Toshiyuki and Piero Carninci (RIKEN)

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov

Plate: LHAM10733 row: 0 column: 03  
 High quality sequence stop: 44.  
 Location/Qualifiers

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 /mol\_type="mRNA"

/db\_xref="taxon:9606"  
 /clone="IMAGE:4823642"

/lab\_host="DH10B"

/clone\_1ib="NIH MGC 97"

/note="Organ: testis; Vector: pBluescriptPCr (modified  
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 (gucag); Oligo-dT primed using primer  
 5'-TTTTTTTTTTTTTVA-3', size-selected for average  
 insert size 2.2 kb and normalized to ROT 5. This is a  
 primary library enriched for full-length clones and  
 constructed using the Cap-trapper method (Carninci, in  
 preparation). Library constructed by M. Brownstein  
 (NHGRI/NHGRI, National Institutes of Health). Note: this is  
 a NIH-MGC Library."

## ORIGIN

Query Match 11.0%; Score 16; DB 4; Length 44;  
 Best Local Similarity 100.0%; Pred. No. 1e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 75 CCGCGGCCCCCAAAAA 90  
 Db 33 CCGCGGCCCCCAAAAA 18

RESULT 2  
 AZ479867/c 39 bp DNA linear GSS 04-OCT-2000

LOCUS AZ479867  
 DEFINITION 1M0300H24R Mouse 10kb plasmid UUC1M library Mus musculus genomic  
 clone UUC1M0300H24 R, genomic survey sequence.

ACCESSION AZ479867  
 VERSION AZ479867.1 GI:10640881  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)

## ORGANISM

Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 39)  
 Dunin, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausen, A. and Wright, D., Weiss, R.

Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts

## TITLE

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 Km. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT

84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0300 row: H column: 24  
 Seq primer: CACACAGGAAACGCTATACAC  
 Class: plasmid ends

High quality sequence stop: 39.  
 Location/Qualifiers

## FEATURES

## source

## 1..39

/organism="Mus musculus"  
 /mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="UUC1M0300H24"

/sex="Male"

/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"

/clone\_1ib="Mouse 10kb plasmid UUC1M library"

/note="Vector: pMD22nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD22 (GI:473211419b/AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## ORIGIN

Query Match 10.3%; Score 15; DB 8; Length 39;  
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 GGGCCCCCAAAAAAT 92  
 Db 15 GGGCCCCCAAAAAAT 1

RESULT 3  
 TA21H040 30 bp DNA linear GSS 13-DEC-2000

LOCUS TA21H040  
 DEFINITION T. Brucei sheared genomic DNA clone 21h04, reverse sequence,  
 genomic survey sequence.

ACCESSION TA21H040  
 VERSION TA21H040.1 GI:11844162  
 KEYWORDS GSS.

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 : Search time 152.479 Seconds  
(without alignments)  
5629.394 Million cell updates/sec

Title: US-09-887-941B-9

Perfect score: 145  
Sequence: 1 tgaagcgcgcgcctccctccct.....nnaagttgagcttcctcc 145

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database : N\_Geneseq16Dec04:  
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4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	16	11.0	25	3	AAA74753	Aaa74753 Mouse mam
2	15	10.3	17	2	AAV97665	Aav97665 Human EGF
3	14	9.7	17	6	ABN79943	Abn79943 Human pla
4	14	9.7	17	10	AD152274	Ad152274 Human tum
5	14	9.7	19	11	ADL79854	Adl79854 Human HER
6	14	9.7	19	11	ADL79854	Adl79854 Human HER
7	14	9.7	20	10	ADC64881	Adc64881 Human bet
8	14	9.7	25	9	AC184826	Ac184826 Human m1c
9	14	9.7	30	6	ABF69403	Abf69403 Novel Hel
10	14	9.7	46	5	AAFP6303	Aafp6303 PCR prime
11	14	9.7	50	4	AA131896	Aa131896 Human SNP
12	14	9.7	50	4	AA131897	Aa131897 Human SNP
13	14	9.7	50	4	AA133973	Aa133973 Human SNP
14	13	9.0	13	4	ABC75550	Abc75550 Oligonuc1
15	13	9.0	13	5	ABC75551	Abc75551 Oligonuc1
16	13	9.0	17	3	AAFP6201	Aafp6201 Hammerhea
17	13	9.0	17	10	ACC52384	Aac52384 Human tum
18	13	9.0	18	2	AAQ97331	Aaq97331 Rat Augme
19	13	9.0	19	2	AA158171	Aat58171 Guanosine
20	13	9.0	19	2	AAx24130	Aax24130 HSV-direc

21	13	9.0	19	8	ACA90041	ACA90041 Cardiovas
22	13	9.0	20	2	AAQ82274	Aaq82274 Chromosom
23	13	9.0	20	2	AAT44268	Aat44268 Guanosine
24	13	9.0	20	2	AAT44277	Aat44277 Guanosine
25	13	9.0	20	2	AAT44266	Aat44266 Guanosine
26	13	9.0	20	4	AAS05867	Aas05867 PCR prime
27	13	9.0	20	10	ADP55356	Adp55356 M. intrac
28	13	9.0	20	10	ABZ97868	Abz97868 Human eot
29	13	9.0	20	11	ABD30899	Abd30899 Human eot
30	13	9.0	20	11	ADH70852	Adh70852 Human Vbe
31	13	9.0	20	12	ADJ59743	Adj59743 Oligonuc1
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33	13	9.0	21	2	AAT58170	Aat58170 Guanosine
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35	13	9.0	22	2	AAT44276	Aat44276 Guanosine
36	13	9.0	22	2	AAx24127	Aax24127 HSV-direc
37	13	9.0	22	12	ADH39973	Adh39973 Ampc beta
38	13	9.0	23	2	AAT44267	Aat44267 Guanosine
39	13	9.0	24	3	AAH8069	Aah8069 Mouse OCT
40	13	9.0	24	4	AAH44746	Aah44746 Human RNA
41	13	9.0	24	8	AAD51531	Aad51531 Reverse p
42	13	9.0	24	8	ACA98546	ACA98546 Human cyt
43	13	9.0	25	9	ACT05407	Act05407 Human m1c
44	13	9.0	25	9	ACT90335	Act90335 Human m1c
45	13	9.0	27	3	AAA30698	Aaa30698 Human ETB
46	13	9.0	27	3	ABZ73385	Abz73385 Mutagenic
47	13	9.0	27	10	ADC22671	Adc22671 Human G P
48	13	9.0	27	10	ADH14144	Adh14144 Human GPC
49	13	9.0	28	10	ADB37656	Adb37656 Streptomy
50	13	9.0	31	4	AA130619	Aa130619 Human sin
51	13	9.0	31	8	ACD44022	Ac444022 Human gen
52	13	9.0	31	10	AA165959	Aa165959 PCR prime
53	13	9.0	33	13	ADT89335	Adt89335 Mouse hep
54	13	9.0	33	13	AAZ96561	Aaz96561 T cell an
55	13	9.0	39	3	ABK30376	Abk30376 Human G-P
56	13	9.0	42	6	ABK58749	Abk58749 Corynebac
57	13	9.0	47	3	AAA99036	Aaa99036 Human TGC
58	13	9.0	47	10	ABZ78720	Abz78720 Human oli
59	13	9.0	47	10	ABZ78720	Abz78720 Tumour su
60	13	9.0	48	11	ADL53116	Adl53116 Human NOG
61	13	9.0	50	2	AAQ69691	Aaq69691 Human ste
62	13	9.0	50	2	AAT25471	Aat25471 Human gen
63	13	9.0	50	2	AAx17441	Aax17441 Human ste
64	13	9.0	50	2	AAx17441	Aax17441 Test sequ
65	13	9.0	50	2	AAH25937	Aah25937 Rice geno
66	13	9.0	50	4	ABK82932	Abk82932 DNA bindi
67	13	9.0	50	6	ABZ02017	Abz02017 Human leu
68	13	9.0	50	12	ADP80471	Adp80471 Duplex ol
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70	12	8.3	12	5	AB120958	Ab120958 Oligonuc1
71	12	8.3	12	5	AB178341	Ab178341 Oligonuc1
72	12	8.3	12	5	ABH92958	Abh92958 Oligonuc1
73	12	8.3	12	5	AB149494	Ab149494 Oligonuc1
74	12	8.3	12	5	ABH93588	Abh93588 Oligonuc1
75	12	8.3	12	5	ABH96945	Abh96945 Oligonuc1
76	12	8.3	12	5	AB168173	Ab168173 Oligonuc1
77	12	8.3	12	5	AB177016	Ab177016 Oligonuc1
78	12	8.3	12	5	AB164667	Ab164667 Oligonuc1
79	12	8.3	12	5	AB107563	Ab107563 Oligonuc1
80	12	8.3	12	5	ABH75680	Abh75680 Oligonuc1
81	12	8.3	12	5	ABH01236	Abh01236 Oligonuc1
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89	12	8.3	12	5	ABH01236	Abh01236 Oligonuc1
90	12	8.3	12	5	ABH01236	Abh01236 Oligonuc1
91	12	8.3	12	5	ABH01236	Abh01236 Oligonuc1
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95      12      8.3      13      5      ABR65357      ABR65357 Oligonuc1
96      12      8.3      13      5      ABC69097      ABC69097 Oligonuc1
c 97      12      8.3      14      2      AAV57033      AAV57033 Human NC
c 98      12      8.3      14      12      ADO80078      ADO80078 Human alp
c 99      12      8.3      15      3      AAS53258      Aas53258 Aryl hydr
c 100     12      8.3      16      3      AAs95719      Aas95719 Oligonuc1
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## ALIGNMENTS

## RESULT 1

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AAA74753/C
ID AAA74753 standard; cDNA; 25 BP.
XX
AC AAA74753;
XX
DT 08-JAN-2001 (first entry)
XX
DE Mouse mammary tumour NOS2 cDNA primer #2.
XX
KW Mouse; cationic amino acid transporter protein; CAT2 transporter;
KW antibacterial; immunosuppressive; cytostatic; dermatological;
KW antiinflammatory; antirheumatic; antiarthritic; neuroprotective;
KW immunomodulator; cardiac; cerebroprotective; protozoacide; sepsis;
KW breast cancer; lung cancer; autoimmune disease; cachexia;
KW systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW cerebral malaria; cardiovascular disease; capillary leak syndrome; ss.
XX
OS Mus sp.
XX
PN WO20004766-A1.
XX
PD 03-AUG-2000.
XX
PF 27-JAN-2000; 2000WO-US002041.
XX
PR 27-JAN-1999; 99US-00238972.
XX
PA (RERE-) RES DEV FOUND.
XX
PI Macleod CL;
XX
DR WPI; 2000-491236/43.
XX
FT Inhibiting cationic amino acid transport by using an antisense
PT oligonucleotide directed against CAT2 mRNA, useful for treating sepsis,
PT neoplastic disease (e.g. breast cancer) and autoimmune diseases (e.g.
PT rheumatoid arthritis).
XX
PS Example 25; Page 48; 94pp; English.
XX
CC The present sequence is a primer which was used to clone the NOS2 cDNA
CC probe by RT-PCR from mouse mammary tumour cDNA. This was part of an
CC example to demonstrate the use of an antisense oligonucleotide directed
CC against CAT2 mRNA to inhibit cationic amino acid transport. Cat2 is one
CC of three genes encoding a transport system which mediates the majority of
CC arginine transport in most cells and tissues. Arginine and its transport
CC are essential for the regulated production of nitric oxide. The method is
CC therefore useful for inhibiting the production of nitric oxide. It is
CC also useful for treating a pathophysiological state characterised by
CC production of an undetectable level of nitric oxide. Such conditions
CC include sepsis, neoplastic disease (e.g. breast cancer or lung cancer),
CC autoimmune diseases (e.g. systemic lupus erythematosus, rheumatoid
CC arthritis or multiple sclerosis), cachexia, cerebral malaria,
CC cardiovascular disease, cerebrovascular disease or capillary leak
CC syndrome
XX
SQ Sequence 25 BP; 5 A; 5 C; 7 G; 8 T; 0 U; 0 Other;
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Query Match 11.0%; Score 16; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 92 TTCGAGCTCAAGACC 107
    |||||
Db 25 TTCGAGCTCAAGACC 10
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## RESULT 2

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AAV97665
ID AAV97665 standard; RNA; 17 BP.
XX
AC AAV97665;
XX
DT 17-MAR-1999 (first entry)
XX
DE Human EGF-R target sequence nucleotide position 3843.
XX
KW Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
KW hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
KW cancer; genetic drift; detection; mutation; ss.
XX
OS Homo sapiens.
XX
PN WO9833893-A2.
XX
PD 06-AUG-1998.
XX
PF 14-JAN-1998; 98NO-US000730.
XX
PR 31-JAN-1997; 97US-0036476P.
XX
PR 04-DEC-1997; 97US-00985162.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI (UVAS-) UNIV ASTON.
XX
PI Akhtar S, Fell P, Mcswiggen JA;
XX
DR WPI; 1998-437449/37.
XX
FT Enzymatic nucleic acids - which cleave RNA derived from an epidermal
PT growth factor receptor, useful for inhibiting cell proliferation and for
PT treating cancers.
XX
PS Claim 5; Page 77; 109pp; English.
XX
CC The present invention describes enzymatic nucleic acid molecules (NMs)
CC which specifically cleave RNA derived from an epidermal growth factor
CC receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
CC represent specifically claimed target sequence from human EGF-R. AAV98044
CC to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
CC hairpin ribozymes respectively for human EGF-R. The NMs are useful for
CC cleaving EGF-R RNA in the treatment of a condition associated with EGFR
CC expression levels e.g. to inhibit cell proliferation in the prevention or
CC treatment of cancers. The NMs can also be used as diagnostic tools to
CC examine genetic drift and mutations within diseased cells or to detect
CC the presence of EGF-R RNA in a cell
XX
SQ Sequence 17 BP; 7 A; 5 C; 2 G; 0 T; 3 U; 0 Other;
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Query Match 10.3%; Score 15; DB 2; Length 17;
Best Local Similarity 86.7%; Pred. No. 1.3e+03;
Matches 13; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 103 GAGCCCTAAATATCC 117
    |||||
Db 2 GAGCCCTAAATATCC 16
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## RESULT 3

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ABN79943
ID ABN79943 standard; DNA; 17 BP.
XX
AC ABN79943;
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 889.692 Seconds  
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7897.122 Million cell updates/sec

Title: US-09-887-941B-9

Perfect score: 145  
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Scoring table: OLIGO\_NUC  
Gap0\_60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

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5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	10.3	17	6	AR402105 Sequence
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3	15	10.3	21	9	AF480506 Homo sapi
4	15	10.3	21	9	HSAS50402 Homo sapi
5	15	10.3	21	9	HSAS50403 Homo sapi
6	14	9.7	17	6	AX398166 Sequence
7	14	9.7	17	6	AX739187 Sequence
8	14	9.7	20	6	BD177288 Sulforan
9	14	9.7	30	6	AX793166 Sequence
10	14	9.7	46	6	BD093895 A method
11	14	9.7	50	6	CQ006464 Sequence
12	14	9.7	50	6	CQ006465 Sequence
13	14	9.7	50	6	CQ008541 Sequence
14	13	9.0	17	6	BD258399 Regulator
15	13	9.0	17	6	AX672706 Sequence
16	13	9.0	18	6	AR042396 Sequence
17	13	9.0	18	6	TI6851 Sequence 16
18	13	9.0	18	6	TI5379 Sequence 16
19	13	9.0	18	6	TI6547 Sequence 16

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c 21	13	9.0	20	6	AX127891 Sequence
c 22	13	9.0	20	6	AX139878 Sequence
c 23	13	9.0	24	6	AX643171 Sequence
c 24	13	9.0	27	6	A07481 Nucleotide
c 25	13	9.0	27	6	A07483 Nucleotide
c 26	13	9.0	27	6	A07485 Nucleotide
c 27	13	9.0	27	6	AR308673 Sequence
c 28	13	9.0	31	6	AX249028 Sequence
c 29	13	9.0	33	6	AR123937 Sequence
c 30	13	9.0	39	6	AR123938 Sequence
c 31	13	9.0	40	9	HUMDB09M3
c 32	13	9.0	41	6	AR263968 Sequence
c 33	13	9.0	47	6	AX522757 Sequence
c 34	13	9.0	47	6	BD013381 Novel pro
c 35	13	9.0	47	6	BD013388 Novel pro
c 36	13	9.0	48	6	A07498 Nucleotide
c 37	13	9.0	48	6	A07500 Nucleotide
c 38	13	9.0	48	6	A07502 Nucleotide
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c 40	13	9.0	50	6	I29569 Sequence 44
c 41	13	9.0	50	6	I29569 Sequence 44
c 42	13	9.0	50	6	AR209493 Sequence
c 43	13	9.0	50	6	BD013694 Method of
c 44	13	9.0	14	6	AR300232 Sequence
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c 46	12	8.3	17	6	BD258400 Regulator
c 47	12	8.3	17	6	AX649106 Sequence
c 48	12	8.3	17	6	AX649107 Sequence
c 49	12	8.3	17	6	AX649108 Sequence
c 50	12	8.3	17	6	AX649109 Sequence
c 51	12	8.3	17	6	AX649110 Sequence
c 52	12	8.3	17	6	AX649111 Sequence
c 53	12	8.3	17	6	AX757975 Sequence
c 54	12	8.3	18	6	A14818 Nucleotide
c 55	12	8.3	18	6	CQ876365 Sequence
c 56	12	8.3	19	6	AR292449 Sequence
c 57	12	8.3	20	6	AR049901 Sequence
c 58	12	8.3	20	6	BD183569 Method fo
c 59	12	8.3	20	6	BD266805 Sequence
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c 62	12	8.3	21	6	AR298353 Sequence
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c 66	12	8.3	22	6	AR158132 Sequence
c 67	12	8.3	22	6	AR158312 Sequence
c 68	12	8.3	22	6	BD137791 Protein e
c 69	12	8.3	22	6	I84203 Sequence 1
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c 71	12	8.3	22	6	AR353117 Sequence
c 72	12	8.3	22	6	AR493411 Sequence
c 73	12	8.3	22	6	AX815754 Sequence
c 74	12	8.3	23	6	CQ878634 Sequence
c 75	12	8.3	23	6	AX148278 Sequence
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c 77	12	8.3	23	6	AX921623 Sequence
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c 82	12	8.3	24	6	AX454948 Sequence
c 83	12	8.3	24	6	AX488599 Sequence
c 84	12	8.3	25	6	AR038302 Sequence
c 85	12	8.3	25	6	I58591 Sequence 13
c 86	12	8.3	25	6	AX088796 Sequence
c 87	12	8.3	25	6	AX650610 Sequence
c 88	12	8.3	25	6	AX650611 Sequence
c 89	12	8.3	25	6	AX650612 Sequence
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 99 12 8.3 25 6 AX650622 Sequence  
 100 12 8.3 25 6 AX650623 Sequence

## ALIGNMENTS

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 LOCUS AR402105 17 bp DNA linear PAT 18-DEC-2003  
 DEFINITION Sequence 445 from patent US 6623962.  
 ACCESSION AR402105  
 VERSION AR402105.1 GI:40149555  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.

REFERENCE  
 AUTHORS 1 (bases 1 to 17)  
 TITLE Akhtar,S., Fell,P. and McSwiggen,J.A.  
 JOURNAL Enzymatic nucleic acid treatment of diseases or conditions related  
 to levels of epidermal growth factor receptors  
 PATENT: US 6623962-A 445 23-SEP-2003;  
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 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 GAGCCCTAAATCC 117  
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 Db 2 GAGCCCTAAATCC 16

RESULT 2  
 LOCUS BD067605 17 bp RNA linear PAT 27-AUG-2002  
 DEFINITION Enzymatic nucleic acid treatment of diseases or conditions related  
 to levels of epidermal growth factor receptors.  
 ACCESSION BD067605  
 VERSION BD067605.1 GI:22613208  
 KEYWORDS JP 2001511003-A/445.  
 SOURCE unidentified  
 ORGANISM unidentified

REFERENCE  
 AUTHORS 1 (bases 1 to 17)  
 TITLE Akhtar,S., Fell,P. and McSwiggen,J.A.  
 JOURNAL Enzymatic nucleic acid treatment of diseases or conditions related  
 to levels of epidermal growth factor receptors  
 PATENT: JP 2001511003-A 445 07-AUG-2001;  
 RIBOZYME PHARMACEUTICALS INC,ASTON UNITV  
 OS Unidentified

COMMENT  
 PN JP 2001511003-A/445  
 PD 07-AUG-2001  
 PR 14-JAN-1998 JP 19985132913  
 SAGRIR AKHTAR, PATRICIA FELL, JAMES A MCSWIGGEN PC  
 C12N9/00, C07K14/71  
 CC Strandedness: Single;  
 CC Topology: linear;  
 CC Enzymatic nucleic acid treatment of diseases or conditions CC  
 related to  
 CC levels of epidermal growth factor receptors  
 FH Key Location/Qualifiers

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 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 103 GAGCCCTAAATCC 117  
 ||||||||||||  
 Db 2 GAGCCCTAAATCC 16

RESULT 3  
 LOCUS AF480506 21 bp RNA linear PRI 01-MAY-2002  
 DEFINITION Homo sapiens microRNA mir-108 gene, complete sequence.  
 ACCESSION AF480506  
 VERSION AF480506.1 GI:20378946  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS 1 (bases 1 to 21)  
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 JOURNAL Mourtelatos,Z., Dostie,J., Pauskhin,S., Sharma,A., Charroux,B.,  
 Abel,L., Rappsilber,J., Mann,M. and Dreyfuss,G.  
 TITLE miRNPs: a novel class of ribonucleoproteins containing numerous  
 microRNAs

JOURNAL Genes Dev. 16 (6), 720-728 (2002)  
 MEDLINE 21912064  
 PUBMED 11914277  
 REFERENCE 2 (bases 1 to 21)  
 AUTHORS Mourtelatos,Z.  
 TITLE Direct Submission

JOURNAL Submitted (05-FEB-2002) HHMI, University of Pennsylvania, CRB Room  
 330, 415 Curie Boulevard, Philadelphia, PA 19104-6148, USA  
 FEATURES  
 SOURCE Location/Qualifiers  
 1..21  
 /organism="Homo sapiens"  
 /mol\_type="other RNA"  
 /db\_xref="taxon:9606"  
 1..21  
 /product="microRNA mir-108"

## misc\_RNA

## ORIGIN

Query Match 10.3%; Score 15; DB 9; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 2.9e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 106 CCTTAAATCCTTA 120  
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 Db 16 CCTTAAATCCTTA 2

RESULT 4  
 LOCUS HSA550402 21 bp RNA linear PRI 19-MAR-2003  
 DEFINITION Homo sapiens microRNA mir-108-1.  
 ACCESSION AJ550402  
 VERSION AJ550402.1 GI:29125708  
 KEYWORDS microRNA mir-108-1; mir-108-1 gene; miRNA.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS 1  
 Lim,L.P., Glasner,M.E., Yekta,S., Burge,C.B. and Bartel,D.P.  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.





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C 81 14 5.6 25 24 US-11-036-317-885379 Sequence 885379,
C 82 14 5.6 25 24 US-11-036-317-920082 Sequence 920082,
C 83 14 5.6 25 24 US-11-036-317-936453 Sequence 936453,
C 84 14 5.6 25 24 US-11-036-317-939447 Sequence 939447,
C 85 14 5.6 25 24 US-11-036-317-940566 Sequence 940566,
C 86 14 5.6 25 24 US-11-036-317-941463 Sequence 941463,
C 87 14 5.6 25 24 US-11-036-317-950472 Sequence 950472,
C 88 14 5.6 25 24 US-11-036-317-975299 Sequence 975299,
C 89 14 5.6 25 24 US-11-036-317-981000 Sequence 981000,
C 90 14 5.6 34 18 US-10-470-751-7 Sequence 7, Appl1
C 91 14 5.6 34 18 US-10-504-132-7 Sequence 384, Appl
C 92 14 5.6 50 10 US-09-993-346-384 Sequence 28, Appl
C 93 13 5.2 15 18 US-10-070-415A-28 Sequence 2, Appl
C 94 13 5.2 15 21 US-10-339-175-2 Sequence 2661, Ap
C 95 13 5.2 17 19 US-10-138-674-2661 Sequence 2661, Ap
C 96 13 5.2 17 17 US-10-287-949A-2661 Sequence 170, App
C 97 13 5.2 18 17 US-10-388-360-170 Sequence 3004, Ap
C 98 13 5.2 18 18 US-10-138-674-3004 Sequence 3004, Ap
C 99 13 5.2 18 19 US-10-287-949A-3004 Sequence 49, Appl
C 100 13 5.2 19 15 US-10-224-005-49 Sequence 49, Appl
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## ALIGNMENTS

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RESULT 1
US-10-719-900-122749
; Sequence 122749, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 122749
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-122749
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Best Local Similarity 100.0%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 9 CGAGACGAGTCACAGAGA 25
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US-10-719-900-183214
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; Sequence 183214, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 183214
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-183214
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Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 AGCTTAGCAGAGACA 16
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; Sequence 422910, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 422910
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-422910
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Query Match 6.4%; Score 16; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 6 CGCCTGAGCAGCGC 21
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RESULT 4
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US-10-719-900-554749/c
; Sequence 554749, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002.11.20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 554749
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-554749
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Query Match 6.4%; Score 16; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 19 GAGACGAGTCACAGAGA 4
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RESULT 5
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US-10-719-900-655519
; Sequence 655519, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
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## ALIGNMENTS

## RESULT 1

US-09-396-196G-18026  
; Sequence 18026, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Miltmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 18026  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-18026

## Query Match

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 196 TTGGAGTCATGATGAC 210  
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DB 7 TTGGAGTCATGATGAC 21

## RESULT 2

US-09-396-196G-119467  
; Sequence 119467, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Miltmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 119467  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-396-196G-119467

## Query Match

Best Local Similarity 100.0%; Score 15; DB 4; Length 25;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 129 TGGAGATGCTGTGAG 143  
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DB 9 TGGAGATGCTGTGAG 23

## RESULT 3

US-08-140-349-14/c  
; Sequence 14, Application US/08140349  
; Patent No. 5679512

## GENERAL INFORMATION:

APPLICANT: Laney, Maureen  
APPLICANT: Chen, Yan  
APPLICANT: Ullman, Edwin F.  
APPLICANT: Hahnenberger, Karen M.  
TITLE OF INVENTION: Method for Introducing Defined Sequences  
TITLE OF INVENTION: at the 3' End of Polynucleotides  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Behring Diagnostics Inc.  
STREET: 3403 Yerba Buena Road  
CITY: San Jose  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 95135  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/140,349  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/923,079  
FILING DATE: 31-JUL-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Leitner, Theodore J.  
REGISTRATION NUMBER: 28,319  
REFERENCE/DOCKET NUMBER: 27660 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 852-1091  
TELEFAX: (415) 493-8870  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 40 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULAR TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
ORIGINAL SOURCE:  
ORGANISM: synthetic  
US-08-140-349-14

## Query Match

Best Local Similarity 100.0%; Score 15; DB 1; Length 40;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GGGGGGGCTTTTCTG 36  
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DB 28 GGGGGGGCTTTTCTG 14

## RESULT 4

US-08-475-236-14/c  
; Sequence 14, Application US/08475236  
; Patent No. 5683879  
; GENERAL INFORMATION:  
; APPLICANT: Laney, Maureen  
; APPLICANT: Chen, Yan  
; APPLICANT: Ullman, Edwin F.  
; APPLICANT: Hahnenberger, Karen M.  
; TITLE OF INVENTION: Method for Introducing Defined Sequences  
; TITLE OF INVENTION: at the 3' End of Polynucleotides  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Behring Diagnostics Inc.  
; STREET: 3403 Yerba Buena Road  
; CITY: San Jose



98 11 4.4 38 8 BH792213 SALK 0629  
99 11 4.4 38 9 AJ595806 Arabidops  
c 100 11 4.4 39 8 AZ833920 AZ833920 2M0116014

## ALIGNMENTS

RESULT 1  
LOCUS BU052484 45 bp mRNA linear EST 29-SEP-2003

DEFINITION BU052484 NIBB Mochii normalized Xenopus neurula library Xenopus laevis cDNA clone XL041k15 3', mRNA sequence.

ACCESSION BU052484.1 GI:17498532

VERSION EST.  
KEYWORDS Xenopus laevis (African clawed frog)

SOURCE  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 45)  
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara,Y.

TITLE Expressed genes in X. laevis embryo  
JOURNAL Unpublished (2001)

COMMENT Contact: Tadasu Shin-I  
Center for Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855

FEATURES  
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/dev\_stage="stage 15"  
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http://xenopus.nibb.ac.jp.  
The information of this clone is available through the following URL.

Location/Qualifiers

ORIGIN  
Query Match 6.0%; Score 15; DB 4; Length 45;  
Best Local Similarity 100.0%; Pred. No. 6e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 GGGGGGGCTTTCTG 28

RESULT 2  
LOCUS AU105461 50 bp mRNA linear EST 28-JAN-2004

DEFINITION AU105461 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC02754, mRNA sequence.

ACCESSION AU105461  
VERSION AU105461.1 GI:13554982

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 50)  
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

REFERENCE  
AUTHORS

TITLE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites  
JOURNAL EMBO Rep. 2 (5), 388-393 (2001)  
MEDLINE 21270072  
PUBMED 11375929

COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp  
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES  
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## ORIGIN

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OY 148 GACGAGACGAGGC 161

Db 8 GACGAGACGAGGC 21

RESULT 3  
LOCUS AU105462 50 bp mRNA linear EST 28-JAN-2004

DEFINITION AU105462 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone HRC05718, mRNA sequence.

ACCESSION AU105462  
VERSION AU105462.1 GI:13554983

KEYWORDS EST.  
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 50)  
Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J., Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K., Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.

REFERENCE Diverse transcriptional initiation revealed by fine, large-scale mapping of mRNA start sites  
EMBO Rep. 2 (5), 388-393 (2001)

JOURNAL MEDLINE 21270072  
PUBMED 11375929

COMMENT Contact: Yutaka Suzuki  
Department of Virology  
Institute of Medical Science, University of Tokyo  
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan  
Email: yusuzuki@ims.u-tokyo.ac.jp

Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2), 149-156 (1997).

FEATURES  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="HRC05718"  
/clone\_lib="Sugano Homo sapiens cDNA library"

## ORIGIN

Query Match 5.6%; Score 14; DB 1; Length 50;  
Best Local Similarity 100.0%; Pred. No. 2.2e+04;

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 263.946 Seconds  
(without alignments)  
5629.394 Million cell updates/sec

Title: US-09-887-941B-8  
Perfect score: 251  
Sequence: 1 59CG9GCGCGGCGACGCGG.....CGTCCCGCCGCTGTGT 251

Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

N\_Geneseq\_16Dec04:\*  
1: geneseq1980s:\*  
2: geneseq1990s:\*  
3: geneseq2000s:\*  
4: geneseq2001as:\*  
5: geneseq2001bs:\*  
6: geneseq2002as:\*  
7: geneseq2002bs:\*  
8: geneseq2003as:\*  
9: geneseq2003bs:\*  
10: geneseq2003cs:\*  
11: geneseq2003ds:\*  
12: geneseq2004as:\*  
13: geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15	6.0	25	9	AC184515 Human m1c
2	15	6.0	28	12	ADN95072 Human CYP
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4	15	6.0	40	2	AAT97484 Productio
5	15	6.0	40	3	AAZ95304 Polynucle
6	15	5.6	20	12	ADM15539 Human m1c
7	15	5.6	20	12	ADM15583 Human m1c
8	15	5.6	20	12	ADM15587 Human m1c
9	15	5.6	20	12	ADM15577 Human m1c
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16	15	5.6	34	9	ADA37010 Human c1u
17	15	5.6	34	12	ADQ26017 C-Jun-N-t
18	15	5.6	41	6	ABL54610 Human syn
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20	15	5.6	50	2	AAT64096 Human alp

21	14	5.6	50	2	AA17384	AA17384 Test sequ
22	14	5.6	50	6	ABK82875	ABK82875 DNA bindi
23	14	5.6	50	12	AD880414	AD880414 Duplex ol
24	13	5.2	14	12	AD078064	AD078064 Human Mx
25	13	5.2	15	10	ABX08694	ABX08694 Patchogeni
26	13	5.2	15	12	ADL72195	ADL72195 Human nuc
27	13	5.2	15	12	ADM30871	ADM30871 Escherich
28	13	5.2	15	12	ADM30869	ADM30869 Escherich
29	13	5.2	15	12	ADM79790	ADM79790 Human DNA
30	13	5.2	15	12	AD078065	AD078065 Human Mx
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32	13	5.2	17	8	ABT36128	ABT36128 Tumour su
33	13	5.2	18	2	AA173494	AA173494 Mouse flk
34	13	5.2	18	10	ADG89222	ADG89222 Cancer de
35	13	5.2	19	10	ABX08689	ABX08689 Pathogeni
36	13	5.2	19	11	AD015168	AD015168 Human PDG
37	13	5.2	19	11	AD014857	AD014857 Human PDG
38	13	5.2	20	2	AAQ73341	AAQ73341 Anti-HSV-
39	13	5.2	20	2	AAQ61978	AAQ61978 HSV detec
40	13	5.2	20	2	AAQ55818	AAQ55818 HCV detec
41	13	5.2	20	4	AAQ82158	AAQ82158 Chromosom
42	13	5.2	20	4	AAQ19517	AAQ19517 PBADGFP4
43	13	5.2	20	10	ADH94413	ADH94413 Human gen
44	13	5.2	20	10	ABZ98408	ABZ98408 Human ICA
45	13	5.2	20	10	AAQ52184	AAQ52184 Human IFN
46	13	5.2	20	11	ABD31439	ABD31439 Human ICA
47	13	5.2	20	12	ADP82972	ADP82972 Glucose-6
48	13	5.2	20	12	ADJ60258	ADJ60258 Oligonuc1
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51	13	5.2	20	12	ADO45747	ADO45747 Human ol1
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53	13	5.2	21	6	ABN9586	ABN9586 Fungi PCR
54	13	5.2	21	6	AA149177	AA149177 Porcine C
55	13	5.2	21	10	AD839766	AD839766 Porcine C
56	13	5.2	24	2	AAV10799	AAV10799 S. clauv1
57	13	5.2	24	6	ABQ07292	ABQ07292 Oligonuc1
58	13	5.2	24	6	ABQ01685	ABQ01685 Oligonuc1
59	13	5.2	24	6	ABQ07333	ABQ07333 Oligonuc1
60	13	5.2	25	9	AC167124	AC167124 Human m1c
61	13	5.2	25	9	ACK00912	ACK00912 Human m1c
62	13	5.2	25	9	ACK30106	ACK30106 Human m1c
63	13	5.2	25	9	AC105162	AC105162 Human m1c
64	13	5.2	25	9	AC152048	AC152048 Human m1c
65	13	5.2	26	5	AA522046	AA522046 Human COL
66	13	5.2	28	2	AAQ87359	AAQ87359 Human IGM
67	13	5.2	28	2	AAQ92511	AAQ92511 Human IGM
68	13	5.2	28	2	AAV66888	AAV66888 Human imm
69	13	5.2	28	2	AAV37305	AAV37305 PCR prime
70	13	5.2	28	3	AA13317	AA13317 PCR prime
71	13	5.2	30	6	ABK57469	ABK57469 Novel Hel
72	13	5.2	32	2	AAV43798	AAV43798 RT-PCR pr
73	13	5.2	33	6	ABK47960	ABK47960 Human lar
74	13	5.2	36	6	AAQ44531	AAQ44531 Helicobac
75	13	5.2	36	12	ADL70692	ADL70692 Escherich
76	13	5.2	39	12	ADM13507	ADM13507 GFP circr
77	13	5.2	40	2	AAQ29503	AAQ29503 neo13-529
78	13	5.2	40	4	AAV10787	AAV10787 S. clauv1
79	13	5.2	40	4	AA181441	AA181441 PCR prime
80	13	5.2	41	6	ABK47963	ABK47963 Human lar
81	13	5.2	41	6	ABK47962	ABK47962 Human lar
82	13	5.2	41	6	ABZ50624	ABZ50624 Human car
83	13	5.2	42	12	ADP48416	ADP48416 Green flu
84	13	5.2	43	8	ABZ68934	ABZ68934 PCR prime
85	13	5.2	45	2	AAT07617	AAT07617 RT-PCR pr
86	13	5.2	45	2	AAT02625	AAT02625 Primer 26
87	13	5.2	46	12	AD192258	AD192258 Human Mx
88	13	5.2	47	10	AAQ30484	AAQ30484 Oligonuc1
89	13	5.2	47	10	ADP32426	ADP32426 Murine 5'
90	13	5.2	47	12	ADM79787	ADM79787 PCR prime
91	13	5.2	47	12	ADM90556	ADM90556 Mouse 5'
92	13	5.2	50	2	AAQ69580	AAQ69580 Human h1s
93	13	5.2	50	2	AAQ89028	AAQ89028 VEGF 2'-N

c	94	13	5.2	50	2	AAT64042	Human his
c	95	13	5.2	50	2	AAX17330	Test sequ
c	96	13	5.2	50	2	AAX52155	Synthetic
c	97	13	5.2	50	2	AAX52077	Synthetic
c	98	13	5.2	50	2	AAX52068	Synthetic
c	99	13	5.2	50	2	AAX52145	Synthetic
c	100	13	5.2	50	3	AAC25209	Human sec

## ALIGNMENTS

XX	RESULT 1
XX	ACI84515/c
ID	ACI84515 standard; DNA; 25 BP.
AC	ACI84515;
DT	14-OCT-2003 (first entry)
DE	Human microarray DNA oligonucleotide SEQ ID NO 84506.
XX	
KW	EST; ss; probe; expressed sequence tag; microarray; gene expression;
KW	genetic variation; diallelic marker; polymorphism; human;
XX	cross-species comparison.
OS	Homo sapiens.
XX	
PN	US2003104410-A1.
XX	
PD	05-JUN-2003.
XX	
PF	15-MAR-2002; 2002US-00098263.
XX	
PR	16-MAR-2001; 2001US-0276759P.
XX	
PA	(AEPF-) AFFYMETRIX INC.
XX	
PI	Mittmann MP;
XX	
PT	WPI; 2003-567953/53.
PT	
PT	New array of nucleic acid probes, useful for in situ hybridization, in
PT	Southern, Northern or dot-blot hybridization to identify or detect the
PT	sequence or specific mutations of any gene.
XX	
PS	Claim 1; SEQ ID NO 84506; 9pp; English.
XX	
CC	The invention discloses a microarray comprising a plurality of nucleic
CC	acid probes including one of 2,018,500 fully defined sequences, or its
CC	perfect match, perfect mismatch, antisense match or antisense mismatch.
CC	Also disclosed is a method of gene expression analysis. The array is used
CC	in monitoring gene expression levels by hybridisation to a DNA library,
CC	in analysis of genetic variation or in hybridisation of tag-labelled
CC	compounds. The nucleic acid probes are specifically designed for analysis
CC	of at least one target sequence. The method of analysis comprises
CC	hybridising at least one or more nucleic acids to at least two or more
CC	nucleic acid probes and detecting the hybridisation. The nucleic acid
CC	probes are attached to a solid support. The analysis comprises monitoring
CC	gene expression levels, identifying diallelic markers or polymorphisms,
CC	or family members of a gene and a cross-species comparison. Each of the
CC	nucleic acids further comprises a tag sequence. The array of nucleic acid
CC	probes is useful in in situ hybridisation, in Southern, Northern or dot-
CC	blot hybridisation to identify or detect the sequence or specific
CC	mutations of any gene, in mapping the 5' terminus of mRNA molecules by
CC	primer extensions or in screening cDNA or genomic libraries or subclones
CC	for additional subclones containing segments of DNA that have been
CC	isolated and previously sequenced. The sequence presented is one of the
CC	nucleic acid probes incorporated in the microarray. Note: The sequence
CC	data for this patent can also be obtained in electronic format directly
CC	from USPTO at <a href="http://seqdata.uspto.gov/sequence.html">seqdata.uspto.gov/sequence.html</a>
XX	
XX	Sequence 25 BP; 6 A; 4 C; 5 G; 10 T; 0 U; 0 Other;

Best Match	6.0%	Score 15;	DB 9;	Length 25;
Query Similarity	100.0%	Pred. No. 2.6e+03;		
Matches	15;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;
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Db	17	AGTCATGATACCCCAA	3	

**RESULT: 2**

ID ADN95072 standard; DNA; 28 BP.  
AC ADN95072;  
DT 29-JUL-2004 (first entry)  
DE Human CYP2W1 PCR primer SEQ ID NO:7.  
KW cytotoxic; anti-cancer; cytochrome P450 enzyme; CYP2W1; enzyme;  
KW cancer therapy; drug target; lung tumour; colon tumour; ovarian tumour;  
KW cancer; human; PCR; primer; ss.  
OS Homo sapiens.  
SS Synthetic.  
PN WO2004/037282-A1.  
PD 06-MAY-2004.  
PF 24-OCT-2003; 2003WO-SEQ01652.  
PX 24-OCT-2002; 2002SE-00003137.  
PR 24-OCT-2002; 2002US-0420787P.  
XX (KARO-) KAROLINSKA INNOVATIONS AB.  
PA Ingelman-Sundberg M, Karlgren M, Gomez A;  
PI WPL; 2004-389744/36.  
DR  
XX New compound comprising a part conferring cytotoxic and/or anti-cancer  
PT effects, and one part conferring binding affinity towards cytochrome P450  
PT enzyme CYP2W1 to the compound, useful in screening agents for treating  
PT cancer.  
XX  
PS Disclosure; SEQ ID NO 7; 46bp; English.  
XX  
CC The present invention describes a compound (1) comprising one part  
CC conferring cytotoxic and/or anti-cancer effects to the compound and one  
CC part conferring binding affinity towards cytochrome P450 enzyme CYP2W1 to  
CC the compound. Also described: (1) a pharmaceutical composition comprising  
CC (1), and pharmaceutical excipients and/or carrier; (2) an antibody,  
CC preferably a monoclonal antibody, binding specifically to CYP2W1; (3) a  
CC DNA molecule having a 137 bp nucleotide sequence of SEQ ID NO:10  
CC (ADN95075); and (4) a method of providing therapeutic agents for cancer  
CC therapy, comprising screening for such agents by using CYP2W1 as a drug  
CC target, or screening for such agents modulating expression of genes  
CC regulated by the CYP2W1 promoter comprising SEQ ID NO:10. The cytochrome  
CC P450 enzyme CYP2W1 and its genetic variants are useful as a drug target  
CC in cancer therapy, preferably in the treatment of lung tumours, colon  
CC tumours and/or ovarian tumours. The substance activated by the enzyme  
CC CYP2W1 and/or inducing the enzyme CYP2W1, and/or the compound above, is  
CC useful for treating cancer. The DNA is useful in the manufacture of a  
CC medicament. The cytochrome P450 form, CYP2W1, has recently been found to  
CC be mainly expressed in tumour cells and is so can be a new potential  
CC agent for effective cancer therapy by acting as a drug target. By  
CC targeting cancer products to CYP2W1, they can be metabolically activated  
CC by the enzyme into the cytotoxic form and reduce unwanted systemic  
CC effects of toxic drugs. The present sequence represents a PCR primer for  
CC human CYP2W1, which is used in the exemplification of the present  
CC invention.

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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 1540.09 Seconds  
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Title: US-09-887-941B-8

Perfect score: 251

Sequence: 1 ggcgggcctggcaccgcgg.....cgttccccaccgtgtgtc 251

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Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

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12: gb\_sy:.\*  
13: gb\_un:.\*  
14: gb\_vi:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 2	15	6.0	40	6	172157
C 3	14	5.6	30	6	126210
C 4	14	5.6	30	7	PPDFRGEMNA
C 5	14	5.6	34	6	BD173847
C 6	14	5.6	50	6	AR032772
C 7	14	5.6	50	6	129512
C 8	14	5.6	50	6	AR209436
C 9	14	5.6	50	6	AR209436
C 10	13	5.2	15	6	BD178522
C 11	13	5.2	15	6	BD182915
C 12	13	5.2	17	6	AR190307
C 13	13	5.2	17	6	AR325259
C 14	13	5.2	17	6	AX730131
C 15	13	5.2	18	6	AR190756
C 16	13	5.2	18	6	AR325602
C 17	13	5.2	19	6	BD178517
C 18	13	5.2	19	6	BD182910
C 19	13	5.2	20	6	AR066810

C 20	13	5.2	20	6	AR074325	AR074325 Sequence
C 21	13	5.2	20	6	E06084	E06084 Oligonucleo
C 22	13	5.2	20	6	120438	120438 Sequence 17
C 23	13	5.2	20	6	AR336961	AR336961 Sequence
C 24	13	5.2	20	6	AX032687	AX032687 Sequence
C 25	13	5.2	20	6	AX237000	AX237000 Sequence
C 26	13	5.2	21	6	AR210246	AR210246 Sequence
C 27	13	5.2	21	6	AX402674	AX402674 Sequence
C 28	13	5.2	24	6	A72149	A72149 Sequence 22
C 29	13	5.2	24	6	AX445237	AX445237 Sequence
C 30	13	5.2	28	6	AR017922	AR017922 Sequence
C 31	13	5.2	28	6	112043	112043 Sequence 8
C 32	13	5.2	30	6	AX791232	AX791232 Sequence
C 33	13	5.2	32	6	AR080472	AR080472 Sequence
C 34	13	5.2	32	6	BD071096	BD071096 Method fo
C 35	13	5.2	40	6	A72137	A72137 Sequence 10
C 36	13	5.2	40	6	AR429928	AR429928 Sequence
C 37	13	5.2	40	6	AX099682	AX099682 Sequence
C 38	13	5.2	43	6	AX769598	AX769598 Sequence
C 39	13	5.2	45	6	155028	155028 Sequence 52
C 40	13	5.2	50	6	AR032718	AR032718 Sequence
C 41	13	5.2	50	6	CQ003456	CQ003456 Sequence
C 42	13	5.2	50	6	CQ003457	CQ003457 Sequence
C 43	13	5.2	50	6	CQ008424	CQ008424 Sequence
C 44	13	5.2	50	6	CQ008633	CQ008633 Sequence
C 45	13	5.2	50	6	CQ008634	CQ008634 Sequence
C 46	13	5.2	50	6	CQ008672	CQ008672 Sequence
C 47	13	5.2	50	6	129458	129458 Sequence 33
C 48	13	5.2	50	6	191132	191132 Sequence 33
C 49	13	5.2	50	6	AR209382	AR209382 Sequence
C 50	13	5.2	50	6	AR282106	AR282106 Sequence
C 51	13	5.2	50	6	AR282117	AR282117 Sequence
C 52	13	5.2	50	6	AR282174	AR282174 Sequence
C 53	13	5.2	50	6	AR282184	AR282184 Sequence
C 54	13	5.2	50	6	AX165027	AX165027 Sequence
C 55	13	5.2	50	6	AX204219	AX204219 Sequence
C 56	13	5.2	50	6	AX913421	AX913421 Sequence
C 57	13	5.2	50	6	BD048954	BD048954 Sequence
C 58	13	5.2	15	6	BD238450	BD238450 Nucleic a
C 59	12	4.8	15	6	AR477142	AR477142 Sequence
C 60	12	4.8	15	6	AR477143	AR477143 Sequence
C 61	12	4.8	15	6	AX019392	AX019392 Sequence
C 62	12	4.8	17	6	CQ618082	CQ618082 Sequence
C 63	12	4.8	17	6	CQ618083	CQ618083 Sequence
C 64	12	4.8	17	6	CQ618084	CQ618084 Sequence
C 65	12	4.8	17	6	CQ618085	CQ618085 Sequence
C 66	12	4.8	17	6	CQ618086	CQ618086 Sequence
C 67	12	4.8	17	6	CQ618087	CQ618087 Sequence
C 68	12	4.8	17	6	AR459145	AR459145 Sequence
C 69	12	4.8	17	6	AR459146	AR459146 Sequence
C 70	12	4.8	17	6	AR459147	AR459147 Sequence
C 71	12	4.8	17	6	AR459148	AR459148 Sequence
C 72	12	4.8	17	6	AR459149	AR459149 Sequence
C 73	12	4.8	17	6	AR459150	AR459150 Sequence
C 74	12	4.8	17	6	AX578501	AX578501 Sequence
C 75	12	4.8	17	6	AX579132	AX579132 Sequence
C 76	12	4.8	17	6	AX579133	AX579133 Sequence
C 77	12	4.8	17	6	AX579472	AX579472 Sequence
C 78	12	4.8	17	6	AX579931	AX579931 Sequence
C 79	12	4.8	17	6	AX725875	AX725875 Sequence
C 80	12	4.8	18	6	AX922556	AX922556 Sequence
C 81	12	4.8	19	6	CQ819476	CQ819476 Sequence
C 82	12	4.8	20	6	AR074324	AR074324 Sequence
C 83	12	4.8	20	6	AR138825	AR138825 Sequence
C 84	12	4.8	20	6	BD264401	BD264401 Growth fa
C 85	12	4.8	20	6	CQ809666	CQ809666 Sequence
C 86	12	4.8	20	6	120437	120437 Sequence 16
C 87	12	4.8	20	6	AR255954	AR255954 Sequence
C 88	12	4.8	20	6	AR261621	AR261621 Sequence
C 89	12	4.8	20	6	AR282981	AR282981 Sequence
C 90	12	4.8	20	6	AR315574	AR315574 Sequence
C 91	12	4.8	20	6	AR430366	AR430366 Sequence
C 92	12	4.8	20	6	AR565718	AR565718 Sequence



C 93 12 4.8 20 6 AX032586  
94 12 4.8 20 6 AX118793  
C 95 12 4.8 20 6 BD096092  
C 96 12 4.8 20 11 DOGCOL10AB  
97 12 4.8 21 6 BD226676  
98 12 4.8 21 6 AR306778  
99 12 4.8 21 6 AR411352  
100 12 4.8 21 6 AX394247  
AX394247 Sequence

## ALIGNMENTS

RESULT 1  
LOCUS 170176 40 bp DNA linear PAT 02-APR-1998  
DEFINITION Sequence 14 from patent US 5679512.  
ACCESSION 170176  
VERSION 170176.1 GI:3006311  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 40)  
AUTHORS Laney,M., Chen,Y., Ullman,E.F. and Hahnenberger,K.M.  
TITLE Method for introducing defined sequences at the 3' end of polynucleotides  
JOURNAL Patent: US 5679512-A 14 21-OCT-1997;  
FEATURES  
source 1..40  
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Query Match 6.0%; Score 15; DB 6; Length 40;  
Best Local Similarity 100.0%; Pred.No. 5.1e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 GGGGGGCTTTCTG 36  
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Db 28 GGGGGGCTTTCTG 14

RESULT 2  
LOCUS 172157 40 bp DNA linear PAT 03-APR-1998  
DEFINITION Sequence 14 from patent US 5683879.  
ACCESSION 172157  
VERSION 172157.1 GI:3008296  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 40)  
AUTHORS Laney,M., Chen,Y., Ullman,E.F. and Hahnenberger,K.M.  
TITLE Method for producing a single stranded polynucleotide having two different defined sequences and kits  
JOURNAL Patent: US 5683879-A 14 04-NOV-1997;  
FEATURES  
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/mol\_type="unassigned DNA"

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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 GGGGGGCTTTCTG 36  
|||||  
Db 28 GGGGGGCTTTCTG 14

RESULT 3  
LOCUS 126210 30 bp DNA linear PAT 07-OCT-1996  
DEFINITION Sequence 7 from patent US 5556953.  
ACCESSION 126210  
VERSION 126210.1 GI:1606080  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 30)  
AUTHORS Zhang,L., Vijay,H.M. and Rode,H.  
TITLE Allergen of drosophila herbarium  
JOURNAL Patent: US 5556953-A 7 17-SEP-1996;  
FEATURES  
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## ORIGIN

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 187 GACGGTGTGCTTGC 200  
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Db 24 GACGGTGTGCTTGC 11

RESULT 4  
LOCUS PPDFRGMENA 30 bp DNA linear PHG 02-APR-1996  
DEFINITION Bacteriophage fd (clone RDEC29) DNA fragment.  
ACCESSION L07985  
VERSION L07985.1 GI:1246245  
KEYWORDS

SOURCE Enterobacteria phage fd  
ORGANISM Enterobacteria phage fd  
REFERENCE 1 (bases 1 to 30)  
AUTHORS Degraef,M.E., Miceli,R.M., Mott,J.E. and Fischer,H.D.  
TITLE Biochemical diversity in a phage display library of random decapeptides  
JOURNAL Gene 128 (1), 13-17 (1993)  
MEDLINE 93285461  
PUBMED 8508954

COMMENT Original source text: Coliphage fd (clone: RDEC29) DNA.  
FEATURES  
source 1..30  
/organism="Enterobacteria phage fd"  
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/clone="RDEC29"

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Best Local Similarity 100.0%; Pred.No. 2.1e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 155 ACAGGGCATGGCAC 168  
|||||  
Db 29 ACAGGGCATGGCAC 16

RESULT 5  
LOCUS BD173847 34 bp DNA linear PAT 18-FEB-2003  
DEFINITION JNK inhibitor.  
ACCESSION BD173847  
VERSION BD173847.1 GI:28415180  
KEYWORDS WO 02062792-A/7;  
SOURCE synthetic construct  
ORGANISM

synthetic construct

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	14	3.9	17	4	US-09-685-664B-2586
4	14	3.9	20	4	US-09-269-446D-127
5	14	3.9	21	3	US-08-430-225A-13
6	14	3.9	21	4	US-09-795-380-13
7	14	3.9	25	4	US-09-396-196G-5566
8	14	3.9	25	4	US-09-396-196G-5567
9	14	3.9	25	4	US-09-396-196G-11905
10	14	3.9	25	4	US-09-396-196G-11906
11	14	3.9	25	4	US-09-396-196G-33457
12	14	3.9	25	4	US-09-396-196G-44285
13	14	3.9	25	4	US-09-396-196G-104809
14	14	3.9	25	4	US-09-396-196G-104810
15	14	3.9	25	4	US-09-396-196G-104826
16	14	3.9	25	4	US-09-396-196G-106629
17	14	3.9	25	4	US-09-396-196G-106630
18	14	3.6	20	1	US-07-977-284A-163
19	14	3.6	20	2	US-08-256-426B-163
20	14	3.6	20	2	US-09-851-062-53
21	14	3.6	20	4	US-09-706-197-64
22	14	3.6	20	4	US-09-422-978-9832
23	14	3.6	20	4	US-09-198-452A-6498
24	14	3.6	20	4	US-09-966-451-62
25	14	3.6	21	1	US-07-937-609-5
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27	14	3.6	21	4	US-09-339-922A-111

C 28	13	3.6	21	4	US-09-443-745-5	Sequence 5, Appli
C 29	13	3.6	21	4	US-09-492-361-25	Sequence 25, Appli
C 30	13	3.6	24	3	US-09-079-984A-4	Sequence 4, Appli
C 31	13	3.6	24	4	US-09-390-729-4	Sequence 4, Appli
C 32	13	3.6	25	1	US-07-924-063A-8	Sequence 8, Appli
C 33	13	3.6	25	4	US-09-396-196G-985	Sequence 985, App
C 34	13	3.6	25	4	US-09-396-196G-986	Sequence 986, App
C 35	13	3.6	25	4	US-09-396-196G-987	Sequence 987, App
C 36	13	3.6	25	4	US-09-396-196G-5003	Sequence 5003, Ap
C 37	13	3.6	25	4	US-09-396-196G-5568	Sequence 5568, Ap
C 38	13	3.6	25	4	US-09-396-196G-13277	Sequence 13277, A
C 39	13	3.6	25	4	US-09-396-196G-15949	Sequence 15949, A
C 40	13	3.6	25	4	US-09-396-196G-20968	Sequence 20968, A
C 41	13	3.6	25	4	US-09-396-196G-20969	Sequence 20969, A
C 42	13	3.6	25	4	US-09-396-196G-39482	Sequence 39482, A
C 43	13	3.6	25	4	US-09-396-196G-49846	Sequence 49846, A
C 44	13	3.6	25	4	US-09-396-196G-67091	Sequence 67091, A
C 45	13	3.6	25	4	US-09-396-196G-69758	Sequence 69758, A
C 46	13	3.6	25	4	US-09-396-196G-70185	Sequence 70185, A
C 47	13	3.6	25	4	US-09-396-196G-77743	Sequence 77743, A
C 48	13	3.6	25	4	US-09-396-196G-77754	Sequence 77754, A
C 49	13	3.6	25	4	US-09-396-196G-93401	Sequence 93401, A
C 50	13	3.6	25	4	US-09-396-196G-94954	Sequence 94954, A
C 51	13	3.6	25	4	US-09-396-196G-94955	Sequence 94955, A
C 52	13	3.6	25	4	US-09-396-196G-94956	Sequence 94956, A
C 53	13	3.6	25	4	US-09-396-196G-108508	Sequence 108508, A
C 54	13	3.6	25	4	US-09-396-196G-123447	Sequence 123447, A
C 55	13	3.6	25	4	US-09-396-196G-125259	Sequence 125259, A
C 56	13	3.6	28	3	US-08-848-760B-23	Sequence 23, Appli
C 57	13	3.6	28	4	US-09-826-025-23	Sequence 23, Appli
C 58	13	3.6	30	1	US-08-384-708A-48	Sequence 48, Appli
C 59	13	3.6	30	3	US-08-687-421-48	Sequence 48, Appli
C 60	13	3.6	30	4	US-09-549-872B-37	Sequence 37, Appli
C 61	13	3.6	30	4	US-08-442-423-48	Sequence 48, Appli
C 62	13	3.6	33	1	US-08-196-922A-43	Sequence 22, Appli
C 63	13	3.6	33	4	US-09-339-922A-83	Sequence 43, Appli
C 64	13	3.6	33	4	US-09-016-061-43	Sequence 83, Appli
C 65	13	3.6	33	4	US-09-016-061-83	Sequence 83, Appli
C 66	13	3.6	34	4	US-09-266-805-13	Sequence 13, Appli
C 67	13	3.6	36	1	US-07-640-029-12	Sequence 12, Appli
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C 69	13	3.6	36	1	US-07-921-807B-18	Sequence 18, Appli
C 70	13	3.6	36	1	US-08-441-944A-18	Sequence 18, Appli
C 71	13	3.6	36	3	US-08-439-992A-12	Sequence 12, Appli
C 72	13	3.6	38	3	US-09-806-254-24	Sequence 24, Appli
C 73	13	3.6	39	3	US-09-079-984A-8	Sequence 8, Appli
C 74	13	3.6	39	3	US-09-306-998-67	Sequence 67, Appli
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C 76	13	3.6	40	4	US-09-715-521C-16	Sequence 16, Appli
C 77	13	3.6	42	2	US-08-701-124-41	Sequence 40, Appli
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C 80	13	3.6	42	3	US-09-130-225-41	Sequence 41, Appli
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C 82	13	3.6	42	3	US-09-306-405-25	Sequence 25, Appli
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C 84	13	3.6	42	3	US-09-306-405-72	Sequence 72, Appli
C 85	13	3.6	42	3	US-09-455-061-40	Sequence 40, Appli
C 86	13	3.6	42	3	US-09-455-061-41	Sequence 41, Appli
C 87	13	3.6	42	4	US-09-969-192-40	Sequence 40, Appli
C 88	13	3.6	44	4	US-09-969-192-41	Sequence 41, Appli
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C 90	13	3.6	44	1	US-08-122-433-11	Sequence 11, Appli
C 91	13	3.6	46	4	US-09-339-159B-53	Sequence 53, Appli
C 92	13	3.6	47	4	US-09-422-978-913	Sequence 913, App
C 93	13	3.6	48	2	US-08-701-124-38	Sequence 38, Appli
C 94	13	3.6	48	3	US-09-130-225-38	Sequence 38, Appli
C 95	13	3.6	48	3	US-09-455-061-38	Sequence 38, Appli
C 96	13	3.6	48	3	US-09-969-192-38	Sequence 38, Appli
C 97	13	3.6	50	1	US-08-171-189-407	Sequence 407, App
C 98	13	3.6	50	1	US-08-171-189-407	Sequence 407, App
C 99	13	3.6	50	2	US-08-123-926-407	Sequence 407, App
C 100	13	3.6	50	2	US-08-475-228A-407	Sequence 407, App

## ALIGNMENTS

RESULT 1  
US-08-584-040-5702  
Sequence 5702, Application US/08584040  
Patent No. 6346398  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pamela  
APPLICANT: McSwigen, James  
APPLICANT: Stinchcomb, Dan T.  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: METHOD AND REAGENT FOR THE  
TREATMENT OF DISEASES OR  
TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS  
TITLE OF INVENTION: OF VASCULAR ENDOTHELIAL  
GROWTH FACTOR  
NUMBER OF SEQUENCES: 8502  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 633 West Fifth Street  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 MB  
MEDIUM TYPE: Storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: Word Perfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/584,040  
FILING DATE: January 11, 1996  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/005,974  
FILING DATE: October 26, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 218/064  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 5702:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-584-040-5702

Query Match 3.9%; Score 14; DB 3; Length 17;  
Best Local Similarity 85.7%; Pred. No. 2.4e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 248 TGAACCTAGAGAAA 261  
DB 2 UGAAACUAGGAAAA 15

RESULT 2  
US-09-371-772B-2586  
Sequence 2586, Application US/09371772B  
Patent No. 6586127  
GENERAL INFORMATION:  
APPLICANT: Ribozyne Pharmaceuticals, Inc.  
APPLICANT: Pavco, Pam

APPLICANT: McSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel  
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: MEHB00,876-J (237/198)  
CURRENT APPLICATION NUMBER: US/09/371,772B  
CURRENT FILING DATE: 1999-08-10  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08  
NUMBER OF SEQ ID NOS: 14225  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2586  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Mus sp.  
US-09-371-772B-2586

Query Match 3.9%; Score 14; DB 4; Length 17;  
Best Local Similarity 85.7%; Pred. No. 2.4e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 248 TGAACCTAGAGAAA 261  
DB 2 UGAAACUAGGAAAA 15

RESULT 3  
US-09-685-664B-2586  
Sequence 2586, Application US/09685664B  
Patent No. 6818447  
GENERAL INFORMATION:  
APPLICANT: Pavco, Pam  
APPLICANT: McSwigen, Jim  
APPLICANT: Stinchcomb, Dan  
APPLICANT: Escobedo, Jaime  
TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Related  
TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor  
FILE REFERENCE: MEHB00-876-K (400/022)  
CURRENT APPLICATION NUMBER: US/09/685,664B  
CURRENT FILING DATE: 2000-10-10  
PRIOR APPLICATION NUMBER: US 60/005,974  
PRIOR FILING DATE: 1995-10-26  
PRIOR APPLICATION NUMBER: US 08/584,040  
PRIOR FILING DATE: 1996-01-08  
PRIOR APPLICATION NUMBER: US 09/371,772  
PRIOR FILING DATE: 1999-08-10  
NUMBER OF SEQ ID NOS: 8231  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2586  
LENGTH: 17  
TYPE: RNA  
ORGANISM: Mus musculus  
US-09-685-664B-2586

Query Match 3.9%; Score 14; DB 4; Length 17;  
Best Local Similarity 85.7%; Pred. No. 2.4e+03;  
Matches 12; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 248 TGAACCTAGAGAAA 261  
DB 2 UGAAACUAGGAAAA 15

RESULT 4  
US-09-269-446D-127  
Sequence 127, Application US/09269446D  
Patent No. 6825332  
GENERAL INFORMATION:  
APPLICANT: Frants, Rune Robert Isak Erik

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:22:30 ; Search time 2497.01 Seconds  
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Title: US-09-887-941B-7

Perfect score: 359  
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Scoring table: OLIGO NUC  
Gapop 60.0, Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 0

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database:

EST:  
1: gb\_est1:  
2: gb\_est2:  
3: gb\_hic:  
4: gb\_est3:  
5: gb\_est4:  
6: gb\_est5:  
7: gb\_est6:  
8: gb\_gsa1:  
9: gb\_gsa2:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	3.6	27	8	BZ354127	SLUK_1232
6	3.6	30	9	AG199320	Pan trogl
7	3.6	30	9	AL946879	Arabidops
8	3.6	31	9	TA9D04F	Alu51921 T. brucei
9	3.6	32	8	BH908757	SLUK_0504
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19	3.3	25	1	AU257461	AU257461
20	3.3	25	1	CG708283	CG708283
21	3.3	27	5	BQ592300	E012698-0
22	3.3	27	7	CF305535	CD1--01-
23	3.3	29	6	CA851403	D13D05_G0
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26	12	3.3	31	1	AI032592	ow73g08.s
27	12	3.3	31	9	CG719539	1119058A1
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32	12	3.3	37	7	AA877091	ob09c09.s
33	12	3.3	37	7	H28311	Y160d11.s1
34	12	3.3	37	8	AZ366273	IM0151L16
35	12	3.3	37	8	AZ663202	IM0542P08
36	12	3.3	38	8	AZ775203	2M0007C24
37	12	3.3	39	8	AZ450000	IM0246H06
38	12	3.3	40	1	AA848120	oe05a03.s
39	12	3.3	40	1	AA887375	o135g08.s
40	12	3.3	40	9	AG203784	Pan trogl
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46	12	3.3	43	9	AL762950	Arabidops
47	12	3.3	43	9	AL762950	Arabidops
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49	12	3.3	44	4	AZ663219	IM0542D17
50	12	3.3	45	7	CF297420	30DGS--08
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54	12	3.3	45	9	BX572448	Arabidops
55	12	3.3	45	9	BX948798	Arabidops
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57	12	3.3	46	1	AA037870	zE04d10.r
58	12	3.3	47	8	AJ590825	Arabidops
59	12	3.3	47	8	AZ819715	2M0091C04
60	12	3.3	47	8	AZ868322	2M0180E01
61	12	3.3	48	9	AX948498	Arabidops
62	12	3.3	48	9	AZ355949	IM0095P17
63	12	3.3	48	9	CL528682	ASV2B12.f
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66	12	3.3	50	1	AU103046	AC0211.sa
67	12	3.3	50	1	AU103046	AU102502
68	12	3.3	50	1	AU103047	AU103043
69	12	3.3	50	1	AU104837	AU103046
70	12	3.3	50	1	AU104837	AU103047
71	12	3.3	50	1	AU105749	AU105749
72	12	3.3	50	1	AU106798	AU106798
73	12	3.3	50	2	BF537767	602054466
74	12	3.3	50	4	BM397711	5009-0-35
75	12	3.3	50	9	CR043171	Reverse.s
76	12	3.1	21	1	AL585535	AL585535
77	12	3.1	21	8	AZ488178	IM00318M13
78	12	3.1	21	8	AZ796205	2M0051O13
79	12	3.1	21	9	AG194016	AG194016
80	12	3.1	22	1	AI153141	Pan trogl
81	12	3.1	22	8	AZ304010	u055a10.r
82	12	3.1	22	8	AZ623308	IM0003O23
83	12	3.1	22	8	AZ623308	IM00460F21
84	12	3.1	23	4	AG195077	AZ2976330
85	12	3.1	23	4	AG195077	2M0251P08
86	12	3.1	24	8	AZ429657	IM0213A16
87	12	3.1	24	8	AZ429657	IM0213A16
88	12	3.1	24	8	AZ784559	IM0236O04
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90	12	3.1	26	1	AU255658	2M0027F20
91	12	3.1	26	8	AZ404703	IM0573P06
92	12	3.1	26	8	AZ404703	IM0573P06
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95	12	3.1	27	1	AU255344	IM0547D11
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98	12	3.1	27	8	BH814090	SAUK_0657
99	12	3.1	27	8	BH856785	SAUK_0791

98 11 3.1 27 9 AG195526  
 C 99 11 3.1 27 9 TA128C06P AL64342 T. brucei  
 100 11 3.1 27 9 CC887313 CC887313 SALK\_1499

## ALIGNMENTS

RESULT 1  
 LOCUS AZ647300/c 43 bp DNA linear GSS 14-DEC-2000  
 DEFINITION 1M051B15R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
 clone UGCGM0513B15 R, genomic survey sequence.

ACCESSION AZ647300  
 VERSION AZ647300.1 GI:11778628  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 43)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plates: 0513 row: B column: 15  
 Seq primer: CACACAGGAAACACGTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 43.

FEATURES  
 source  
 1. .43  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCGM0513B15"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCGM library"  
 /note="Vector: PWD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PWD42 (g114732114[gblAF129072.1]), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

ORIGIN  
 Query Match 4.2%; Score 15; DB 8; Length 43;

Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 333 GTTCTCATCACCCTGC 347  
 Db 36 GTTCTCATCACCCTGC 22

RESULT 2  
 LOCUS AA909441 31 bp mRNA linear EST 10-JUN-1998  
 DEFINITION 0114c09.g1 Soares NFL T GBC S1 Homo sapiens cDNA clone  
 IMAGE:1523440 3' similar to TR:035606 O35606 HYPOTHETICAL 35.7 KD  
 PROTEIN ; mRNA sequence.

ACCESSION AA909441  
 VERSION AA909441.1 GI:3048846  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 31)  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Project (CGAP),  
 Tumor Gene Index

JOURNAL Unpublished (1997)  
 COMMENT Contact: Robert Straubeberg, Ph.D.  
 Email: cgapsb-r@mail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Insert length: 645 Std Error: 0.00  
 Seq primer: -40m13 fwd. RT from Amersham  
 High quality sequence stop: 1.  
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 /db\_xref="taxon:9606"  
 /clone="IMAGE:1523440"  
 /lab\_host="DH10B"  
 /lab\_host="Soares\_NFL\_T\_GBC\_S1"  
 /note="Organ: pooled; Vector: pRT3D-Pac (Pharmacia) with  
 a modified polylinker; Site 1: Not 1; Site 2: Eco RI;  
 Equal amounts of plasmid DNA from three normalized  
 libraries (fetal lung NBH19w, testis NHT, and B-cell  
 NCI-CCAP-GCB1) were mixed, and ss circles were made in  
 vitro. Following HAP purification, this DNA was used as  
 tracer in a subtractive hybridization reaction. The driver  
 was PCR-amplified cDNAs from pools of 5,000 clones made  
 from the same 3 libraries. The pools consisted of  
 1 M.A.G.E. clones 297480-302087, 682632-687239,  
 726408-728711, and 729096-731399. Subtraction by Bento  
 Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 3.9%; Score 14; DB 1; Length 31;  
 Best Local Similarity 100.0%; Pred. No. 4.4e+04;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 AAGTGAATCAGACA 32  
 Db 4 AAGTGAATCAGACA 17

RESULT 3  
 LOCUS AZ630264 35 bp DNA linear GSS 13-DEC-2000  
 DEFINITION 1M0483P14R Mouse 10kb plasmid UGCGM library Mus musculus genomic  
 clone UGCGM0483P14 R, genomic survey sequence.

ACCESSION AZ630264  
 VERSION AZ630264.1 GI:11752454  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)

PR 08-JAN-2001; 2001US-0260326P.  
 PR 24-JAN-2001; 2001US-0263800P.  
 PR 20-FEB-2001; 2001US-0269942P.  
 PR 24-APR-2001; 2001US-0286183P.  
 PR 20-AUG-2001; 2001US-0313627P.  
 PR 12-SEP-2001; 2001US-0318712P.

XX (CURA-) CURAGEN CORP.

PI Guo X, Li L, Patturajan M, Shinkets RA, Casman SJ, Malpankar UM;  
 PI Tcherev VT, Vernet CM, Spytek KA, Shenoy SG, Alsobrook JP;  
 PI Edinger S, Peyman JA, Stone DJ, Ellerman K, Gangolli EA, Boldog FL;  
 PI Colman SD, Eissen AF, Liu X, Padigaru M, Spaderma SK, Zehusen BD;  
 XX WPI; 2002-547774/58.

XX Novel isolated polypeptide, designated NOVX, useful for treating or  
 PT preventing cancer, diabetes, obesity, dyslipidemia, anorexia, and  
 PT metabolic, neurodegenerative, immune and hematopoietic disorders.

XX Example 2; Page 331; 421pp; English.

XX The invention relates to an isolated polypeptide, designated NOVX,  
 CC comprising a sequence fully defined in the specification. The isolated  
 CC protein, its encoding polynucleotide or an antibody created from the  
 CC protein is useful in the manufacture of a medicament for treating a  
 CC syndrome associated with a human disease, preferably a NOVX-associated  
 CC disorder, or for treating or preventing a NOVX-associated disorder in a  
 CC subject, preferably human. The isolated protein, its encoding  
 CC polynucleotide or an antibody created from the protein are also useful  
 CC for treating or preventing metabolic disorders, diabetes, obesity,  
 CC infectious disease, anorexia, neurodegenerative disorder, Alzheimer's  
 CC disease, Parkinson's disorder, immune disorders, haematopoietic  
 CC disorders, and various dyslipidaemias, metabolic disturbances associated  
 CC with obesity, the metabolic syndrome X, wasting disorders associated with  
 CC chronic diseases, and cancer. The isolated protein, its encoding  
 CC polynucleotide or an antibody created from the protein are useful for  
 CC treating or preventing neurological disorders such as epilepsy, stroke,  
 CC mental disorders including mood, anxiety, schizophrenic disorders,  
 CC disorders of vesicular transport such as cystic fibrosis, diabetes  
 CC mellitus, golfer, gastrointestinal disorders including ulcerative  
 CC colitis, other conditions associated with abnormal vesicle trafficking  
 CC including AIDS, allergic reactions, multiple sclerosis and rheumatoid  
 CC arthritis. A cell comprising the vector of the invention is useful for  
 CC producing non-human transgenic animals. The polynucleotide of the  
 CC invention can be used to treat disorders by gene therapy. This  
 CC polynucleotide sequence represents a probe of a sequence relating to the  
 CC NOVX proteins of the invention

XX Sequence 23 BP; 2 A; 10 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 4.5%; Score 16; DB 6; Length 23;

Best Local Similarity 100.0%; Pred. No. 9.6e+02; Mismatches 0; Gaps 0;

OY 39 TCCCTCCCTGCTGCTG 54  
 DB 8 TCCCTCCCTGCTGCTG 23

RESULT 4  
 ACI09033/c

ID ACI09033 standard; DNA; 25 BP.

XX ACI09033;

XX 13-OCT-2003 (first entry)

XX Human microarray DNA oligonucleotide SEQ ID NO 9024.

XX EST; ss; probe; expressed sequence tag; microarray; gene expression;  
 KW genetic variation; diallelic marker; polymorphism; human;  
 KW cross-species comparison.

XX Homo sapiens.

XX US200104410-A1.

XX 05-JUN-2003.

XX 15-MAR-2002; 2002US-00098263.

XX 16-MAR-2001; 2001US-0276759P.

XX (AFV-) AFFMETRIX INC.

XX Miltmann MP;

XX WPI; 2003-567953/53.

XX New array of nucleic acid probes, useful for in situ hybridization, in  
 PT Southern, Northern or dot-blot hybridization to identify or detect the  
 PT sequence or specific mutations of any gene.

XX Claim 1; SEQ ID NO 9024; 9pp; English.

XX The invention discloses a microarray comprising a plurality of nucleic  
 CC acid probes including one of 2,018,500 fully defined sequences, or its  
 CC perfect match, perfect mismatch, antisense match or antisense mismatch.  
 CC Also disclosed is a method of gene expression analysis. The array is used  
 CC in monitoring gene expression levels by hybridisation to a DNA library,  
 CC in analysis of genetic variation or in hybridisation of tag-labelled  
 CC compounds. The nucleic acid probes are specifically designed for analysis  
 CC of at least one target sequence. The method of analysis comprises  
 CC hybridising at least one or more nucleic acids to at least two or more  
 CC nucleic acid probes and detecting the hybridisation. The nucleic acid  
 CC probes are attached to a solid support. The analysis comprises monitoring  
 CC gene expression levels, identifying diallelic markers or polymorphisms,  
 CC or family members of a gene and a cross-species comparison. Each of the  
 CC nucleic acids further comprises a tag sequence. The array of nucleic acid  
 CC probes is useful in in situ hybridisation, in Southern, Northern or dot-  
 CC blot hybridisation to identify or detect the sequence or specific  
 CC mutations of any gene, in mapping the 5' termini of mRNA molecules by  
 CC primer extensions or in screening cDNA or genomic libraries or subclones  
 CC for additional subclones containing segments of DNA that have been  
 CC isolated and previously sequenced. The sequence presented is one of the  
 CC nucleic acid probes incorporated in the microarray. Note: The sequence  
 CC data for this patent can also be obtained in electronic format directly  
 CC from USPTO at seqdata.uspto.gov/sequence.html

XX Sequence 25 BP; 4 A; 10 C; 3 G; 8 T; 0 U; 0 Other;

Query Match 4.5%; Score 16; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 9.6e+02; Mismatches 0; Gaps 0;

OY 216 TCAGAAAGGCTGAGAG 231  
 DB 16 TCAGAAAGGCTGAGAG 1

RESULT 5  
 ACH56901/c

ID ACH56901 standard; DNA; 25 BP.

XX ACH56901;

XX 16-OCT-2003 (first entry)

XX DNA target sequence #6037 useful in array for genetic analyses.

XX Gene expression analysis; array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;  
 KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KW target sequence; probe; PCR; primer; ss.

XX OS Unidentified.  
 XX PN US2003082596-A1.  
 XX PD 01-MAY-2003.  
 XX PF 08-AUG-2002; 2002US-00215112.  
 XX PR 08-AUG-2001; 2001US-0311040P.  
 XX PA (MITT/) MITTMANN M.  
 XX PI Mittmann M;  
 XX DR WPI; 2003-576608/54.  
 XX PT New probe array useful e.g. for monitoring gene expression levels, for  
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.  
 PS Claim 1; SEQ ID NO 6037; 9pp; English.  
 XX CC The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridising tag-labelled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' termini of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.  
 CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at [seqdata.uspto.gov/patseq/entry.html](http://seqdata.uspto.gov/patseq/entry.html)  
 XX SQ Sequence 25 BP; 8 A; 7 C; 7 G; 3 T; 0 U; 0 Other;  
 XX  
 XX Query Match 4.5%; Score 16; DB 9; Length 25;  
 XX Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 295 ACACACTGCTTCTGCT 310  
 Db 23 ACACACTGCTTCTGCT 8  
 XX  
 XX RESULT 6  
 XX ACH56902/C  
 XX ID ACH56902 standard; DNA; 25 BP.  
 XX AC ACH56902;  
 XX DT 16-OCT-2003 (first entry)  
 XX  
 XX DNA target sequence #6038 useful in array for genetic analyses.  
 XX  
 XX Gene expression analysis: array; hybridisation; genetic variation;  
 KW tag-labelled compound; gene family; in situ hybridisation;  
 KW library screening; Southern hybridisation; northern hybridisation;  
 KW dot-blot hybridisation; gene sequence; mutation detection;  
 KW target sequence; probe; PCR; primer; ss.

XX OS Unidentified.  
 XX PN US2003082596-A1.  
 XX PD 01-MAY-2003.  
 XX PF 08-AUG-2002; 2002US-00215112.  
 XX PR 08-AUG-2001; 2001US-0311040P.  
 XX PA (MITT/) MITTMANN M.  
 XX PI Mittmann M;  
 XX DR WPI; 2003-576608/54.  
 XX PT New probe array useful e.g. for monitoring gene expression levels, for  
 PT analyzing genetic variations, or for hybridizing tag-labeled compounds,  
 PT comprises multiple nucleic acid probes.  
 PS Claim 1; SEQ ID NO 6038; 9pp; English.  
 XX CC The present invention relates to nucleic acid sequences that are  
 CC complementary to particular genes, and can be used as probes for a  
 CC variety of analyses such as gene expression analysis. Each probe  
 CC comprises 9 or more consecutive nucleotides from at least one of 14936  
 CC nucleotide sequences defined in the patent, or their perfect sense match,  
 CC sense mismatch, antisense match or antisense mismatch oligonucleotides.  
 CC The probes may be used in an array comprising at least 10 distinct  
 CC nucleic acid probes. The array is useful in monitoring gene expression  
 CC levels by hybridisation to a DNA library, in analysing genetic  
 CC variations, and in hybridising tag-labelled compounds. The probes are  
 CC useful for identifying family members of a gene. The probes are also  
 CC useful in situ hybridisations, in screening cDNA or genomic libraries  
 CC (or derived subclones) for additional clones containing segments of DNA  
 CC that have been previously isolated and sequenced, in Southern, northern,  
 CC or dot-blot hybridisation of genomic DNA to identify or detect the  
 CC sequence of any gene or detect specific mutations in any gene, and in  
 CC mapping the 5' termini of mRNA molecules by primer extensions. The  
 CC nucleic acid sequences of the invention are also useful as PCR primers.  
 CC The invention provides a large collection of nucleic acid sequences  
 CC complementary to particular genes with a wide range of analytical uses.  
 CC ACH50865-ACH65260 represent the target sequences of the invention. Note:  
 CC The sequence data for this patent was obtained in electronic format  
 CC directly from the USPTO web site at [seqdata.uspto.gov/patseq/entry.html](http://seqdata.uspto.gov/patseq/entry.html)  
 XX SQ Sequence 25 BP; 8 A; 7 C; 7 G; 3 T; 0 U; 0 Other;  
 XX  
 XX Query Match 4.5%; Score 16; DB 9; Length 25;  
 XX Best Local Similarity 100.0%; Pred. No. 9.6e+02;  
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 295 ACACACTGCTTCTGCT 310  
 Db 23 ACACACTGCTTCTGCT 8  
 XX  
 XX RESULT 7  
 XX AD150603  
 XX ID AD150603 standard; DNA; 17 BP.  
 XX AC AD150603;  
 XX DT 15-APR-2004 (first entry)  
 XX  
 XX Human tumour suppression/reversion-related DNA sequence SeqID1106.  
 XX  
 XX tumour suppression; tumour reversion; apoptosis; virus resistance;  
 KW cytoskeletal; virucide; neuroprotective; neurotrophic; neuroleptic; probe;  
 KW primer; PCR; gene chip; antisense; viral disease; tumour;  
 KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.  
 XX

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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 377.516 Seconds  
(without alignments)  
5629.394 Million cell updates/sec

Title: US-09-887-941b-7

Perfect score: 359

Sequence: 1 cccgcggggcgagcaatccaa.....tcacctgcctcgcgcgcg 359

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 295987067 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

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1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	4.7	30	2	AAQ10507
2	16	4.5	20	12	ADK96823
3	16	4.5	23	6	ABT05541
4	16	4.5	23	9	ACT109033
5	16	4.5	25	9	ACH56901
6	16	4.5	25	9	ACH56902
7	15	4.2	17	10	AD150603
8	15	4.2	17	12	AD016727
9	15	4.2	20	6	AA147253
10	15	4.2	48	10	ACH01195
11	15	4.2	48	10	ACH01186
12	15	4.2	50	6	ABZ02647
13	14	3.9	15	2	AAZ54056
14	14	3.9	15	3	AAA33500
15	14	3.9	15	3	AAI19622
16	14	3.9	15	3	ABZ95316
17	14	3.9	15	11	ABD19300
18	14	3.9	17	2	AAZ72952
19	14	3.9	18	4	AAZ08679
20	14	3.9	18	4	AAZ08679

C	21	14	3.9	19	10	ADP37186	Adf37186 Human VEG
C	22	14	3.9	19	10	ADP36862	Adf36862 Human VEG
C	23	14	3.9	20	2	AAV29457	AAV29457 Calcium i
C	24	14	3.9	21	2	AAV40022	AAV40022 Primer fo
C	25	14	3.9	21	6	AAI18347	AAI18347 5'-RACE h
C	26	14	3.9	22	3	AAA66353	AAA66353 Dog genom
C	27	14	3.9	22	3	ABZ79337	ABZ79337 Acetyl-Co
C	28	14	3.9	25	9	ACT18925	ACT18925 Human mtc
C	29	14	3.9	25	9	ACK09568	ACK09568 Human mtc
C	30	14	3.9	25	9	ACK18741	ACK18741 Human mtc
C	31	14	3.9	25	9	ACT182734	ACT182734 Human mtc
C	32	14	3.9	25	9	ACT176389	ACT176389 Human mtc
C	33	14	3.9	28	12	ADN43292	ADN43292 Nucleoeti
C	34	14	3.9	28	12	ADN43291	ADN43291 Nucleoeti
C	35	14	3.9	30	2	AAI10251	AAI10251 Human Fas
C	36	14	3.9	30	12	AAI56358	AAI56358 Human pro
C	37	14	3.9	33	9	ACC49573	ACC49573 Beta-cong
C	38	14	3.9	33	9	AAI56359	AAI56359 Human pro
C	39	14	3.9	41	6	ABX15068	ABX15068 Homeotic
C	40	14	3.9	44	4	AAZ08226	AAZ08226 Human ret
C	41	14	3.9	50	6	AAZ06830	AAZ06830 GPR10/UHR
C	42	14	3.9	50	6	ABZ06631	ABZ06631 Human leu
C	43	14	3.9	50	6	ABZ07021	ABZ07021 Human leu
C	44	14	3.9	15	3	AAA95134	AAA95134 Allele sp
C	45	13	3.6	16	10	ACE63282	ACE63282 Human ATP
C	46	13	3.6	17	2	AAI17247	AAI17247 Aryl hydr
C	47	13	3.6	17	8	ACC65579	ACC65579 Murine ol
C	48	13	3.6	18	6	AAI31555	AAI31555 hp40R1 PC
C	49	13	3.6	18	6	ABL30592	ABL30592 Human HLA
C	50	13	3.6	18	6	ABL31038	ABL31038 Human HLA
C	51	13	3.6	18	12	ADP713176	ADP713176 Anti-RELP
C	52	13	3.6	19	6	ABZ71759	ABZ71759 Human rev
C	53	13	3.6	19	6	ABZ71762	ABZ71762 Human rev
C	54	13	3.6	19	6	ABZ97315	ABZ97315 Aryl hydr
C	55	13	3.6	19	11	ADL36072	ADL36072 Human NOV
C	56	13	3.6	19	11	ADL36075	ADL36075 Human NOV
C	57	13	3.6	19	12	ADH70599	ADH70599 Human Vde
C	58	13	3.6	19	12	ADH72403	ADH72403 Human rev
C	59	13	3.6	19	12	ADH72406	ADH72406 Human rev
C	60	13	3.6	20	2	AAQ65890	AAQ65890 Type II p
C	61	13	3.6	20	2	AAZ32026	AAZ32026 MSH2 gene
C	62	13	3.6	20	2	AAZ97172	AAZ97172 Primer us
C	63	13	3.6	20	3	AAZ75476	AAZ75476 Human bia
C	64	13	3.6	20	4	AAZ62218	AAZ62218 PCR prime
C	65	13	3.6	20	4	AAZ96618	AAZ96618 Human SR-
C	66	13	3.6	20	6	ABZ57886	ABZ57886 Human ABC
C	67	13	3.6	20	8	AAI52108	AAI52108 Escherich
C	68	13	3.6	20	9	ADA45267	ADA45267 Human MSH
C	69	13	3.6	20	10	ADZ66347	ADZ66347 Human col
C	70	13	3.6	20	10	ADZ89431	ADZ89431 AP-1 prob
C	71	13	3.6	20	10	ADZ87540	ADZ87540 Single nu
C	72	13	3.6	20	10	ABZ98647	ABZ98647 Human try
C	73	13	3.6	20	10	ABZ92982	ABZ92982 Human o11
C	74	13	3.6	20	10	ABZ85397	ABZ85397 Human o11
C	75	13	3.6	20	10	ABZ92983	ABZ92983 Human o11
C	76	13	3.6	20	10	ABZ85396	ABZ85396 Human o11
C	77	13	3.6	20	10	ACC58952	ACC58952 Human int
C	78	13	3.6	20	10	ABZ33990	ABZ33990 Human int
C	79	13	3.6	20	11	ABD21627	ABD21627 S100 calc
C	80	13	3.6	20	11	ABD21626	ABD21626 S100 calc
C	81	13	3.6	20	11	ABD29212	ABD29212 AA150500-
C	82	13	3.6	20	11	ABD29213	ABD29213 AA150500-
C	83	13	3.6	20	11	ABD29213	ABD29213 AA150500-
C	84	13	3.6	20	12	ADU60526	ADU60526 Oligonuc1
C	85	13	3.6	20	12	ADU60526	ADU60526 Oligonuc1
C	86	13	3.6	21	2	AAQ47676	AAQ47676 Sequence
C	87	13	3.6	21	3	AAZ46107	AAZ46107 PCR prime
C	88	13	3.6	21	3	AAZ47641	AAZ47641 Intronic
C	89	13	3.6	21	4	AAZ29947	AAZ29947 Primer #5
C	90	13	3.6	21	4	AAZ59986	AAZ59986 Human gen
C	91	13	3.6	21	4	AAH62621	AAH62621 GUCY1B3 p
C	92	13	3.6	21	4	AAH62621	AAH62621 DNA encod
C	93	13	3.6	21	6	ABZ97326	ABZ97326 Aryl hydr



```

C 94 13 3 6 21 9 ACD26205 Adc26205 RACE olig
95 13 3 6 21 10 Adc42650 Human FAN
96 13 3 6 21 12 Adc85723 Human Fph
97 13 3 6 22 2 Adg77609 Canine dl
98 13 3 6 22 12 Ado18066 Ado18066 Primer of
99 13 3 6 22 13 Ado17994 Ado17994 Primer of
100 13 3 6 22 13 Adsl9261 Adsl9261 Protein r

```

## ALIGNMENTS

## RESULT 1

AAQ10507  
ID AAQ10507 standard; DNA; 30 BP.

AC AAQ10507;  
AD

DT 09-APR-1991 (first entry)

DE 5' primer (87-311) for amplification of male-specific bovine DNA.

KW bovine; sex determination; male-specific probe; PCR; ss.

OS Synthetic.

PN WO9100365-A.

PD 10-JAN-1991.

PF 13-JUN-1989; 89US-00366153.

PR 13-JUN-1989; 89US-00366153.

PA (SALK) SALK INST BIOTECHN.

PI Kwok DY, Gingeras T;

DR WPI; 1991-036756/05.

PT Prenatal bovine sex determ. - using male-specific oligo-nucleotide

PS probes, with increased sensitivity.

PS Claim 8; Page 31; 40pp; English.

CC This 5' primer is used in association with a 3' primer (AAQ10508) and a

CC detection oligonucleotide (AAQ10509) in a sex-determination assay. A male

CC -specific segment of bovine DNA is amplified by using the primers in a

CC Polymerase Chain Reaction. The amplified, double-stranded male-specific

CC segment is then detected by hybridisation between the DNA and the

CC specified probe. See also AAQ10504-6 and AAQ10510-18

XX Sequence 30 BP; 10 A; 13 C; 4 G; 3 T; 0 U; 0 Other;

QY Query Match 4.7%; Score 17; DB 2; Length 30;

Db Best Local Similarity 100.0%; Pred. No. 3e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

170 CTGACAAACACTCTCTGA 186

7 CTGACAAACACTCTCTGA 23

RESULT 2

ADK96823/c

ID ADK96823 standard; DNA; 20 BP.

AC ADK96823;

XX 06-MAY-2004 (first entry)

DT Primer of the invention #2543.

DE

XX

KW human; single nucleotide polymorphism; SNP; ss; primer.

OS Synthetic.

PN JP2003259875-A.

PD 16-SEP-2003.

PF 08-MAR-2002; 2002JP-00064373.

PR 08-MAR-2002; 2002JP-00064373.

PA (KAGA-) KAGAKU GIYUSU SHINKO JIGYODAN.

DR WPI; 2004-093977/10.

PT Novel polynucleotide useful for PCR amplification along with two DNA

PT fragment from another set of sequences, or for detecting single

PT nucleotide polymorphism in human gene.

PS Claim 2; SEQ ID NO 5852; 2627bp; Japanese.

CC The present invention relates to a polynucleotide isolated from a human

CC gene and is useful for detecting a single nucleotide polymorphism in a

CC human gene or for diagnosing of disease. The invention enables the

CC detection of a single nucleotide polymorphism in a human gene. The

CC present sequence represents a primer of the invention.

XX Sequence 20 BP; 2 A; 8 C; 4 G; 6 T; 0 U; 0 Other;

QY Query Match 4.5%; Score 16; DB 12; Length 20;

Db Best Local Similarity 100.0%; Pred. No. 9.5e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

142 AGAGGGCACAGATGCT 157

17 AGAGGGCACAGATGCT 2

RESULT 3

ABT05541

ID ABT05541 standard; DNA; 23 BP.

AC ABT05541;

XX 11-OCT-2002 (first entry)

DE NOVX related probe SEQ ID No 215.

XX Cytostatic; antidiabetic; anorectic; metabolic; nootropic; antihypertic;

XX neuroprotective; antiparkinsonian; anticonvulsant; cerebroprotective;

XX tranquiliser; neuroleptic; antidiabetic; antitumor; antiinflammatory;

XX anti-HIV; antiallergic; antirheumatic; antitarditic; NOVX; diabetes;

XX metabolic disorder; obesity; infectious disease; Alzheimer's disease;

XX anorexia; neurodegenerative disorder; Parkinson's disease; obesity;

XX immune disorder; haematopoietic disorder; dyslipidaemia; chronic disease;

XX metabolic syndrome X; wasting disorder; cancer; neurological disorder;

XX epilepsy; stroke; mental disorder; schizophrenic disorders; golfer;

XX vesicular transport; cystic fibrosis; gastrointestinal disorder;

XX diabetes mellitus; ulcerative colitis; AIDS; allergic reaction;

XX multiple sclerosis; rheumatoid arthritis; transgenic animal;

XX gene therapy; probe; ss.

XX Unidentified.

XX OS

XX PN WO200246409-A2.

XX 13-JUN-2002.

XX PD 06-DEC-2001; 2001WO-US046586.

XX PF 06-DEC-2000; 2000US-0251660P.

XX PR 12-DEC-2000; 2000US-0255029P.

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 2202.75 Seconds  
(without alignments)  
7897.122 Million cell updates/sec

Title: US-09-887-941B-7  
Perfect score: 359  
Sequence: 1 cccgcggggcagatccca.....tcactgcctcgcggcgcgc 359

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

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2: gb\_hvg:\*  
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6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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4	14	3.9	17	6	AR325184 Sequence
5	14	3.9	18	6	AX189329 Sequence
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7	14	3.9	20	6	A79290 Sequence 12
8	14	3.9	20	6	BD003520 A gene re
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 ACCESSION AX591854  
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KEYWORDS  
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 ORGANISM  
 REFERENCE  
 AUTHORS

1  
 Guo,X., Li,L., Patturajan,M., Shinkets,R.A., Casman,S.J.,  
 Malyanar,U.M., Tchernev,V.T., Vernet,C.A., Spytek,K.A.,  
 Shenoy,S.G., Alsbrook,J.P., Edinger,S., Peyman,J.A., Stone,D.J.,  
 Ellerman,K., Gangoli,E.A., Boldog,F.L., Colman,S.D., Eisen,A.D.,  
 Liu,X., Padigaru,M., Spaderna,S.K. and Zerhusen,B.D.  
 Proteins and nucleic acids encoding same  
 Patent: WO 0246409-A 215 13-JUN-2002;  
 Curegen Corporation (US)

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 Telemann,A., Amsen,R. and Tuijinder,M.  
 Sequences involved in phenomena of tumour suppression, tumour  
 reversion, apoptosis and/or resistance to viruses and the use  
 thereof as medicaments  
 Patent: WO 03025177-A 3106 27-MAR-2003;  
 Molecular Engines Laboratories (FR)  
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REFERENCE  
 Pavco,P., McSwiggen,J., Stinchcomb,D. and Escobedo,J.  
 Method and reagent for the treatment of diseases or conditions  
 related to levels of vascular endothelial growth factor receptor  
 Patent: US 6346398-A 5702 12-FEB-2002;  
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 Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.  
 Method and reagent for the treatment of diseases or conditions  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 93 13 7.3 21 17 US-10-293-965-20 Sequence 20, Appl
C 94 13 7.3 21 17 US-10-293-965-22 Sequence 22, Appl
C 95 13 7.3 21 17 US-10-293-965-32 Sequence 32, Appl
C 96 13 7.3 21 21 US-10-643-775-570 Sequence 35, Appl
C 97 13 7.3 21 21 US-10-643-775-570 Sequence 35, Appl
C 98 13 7.3 21 22 US-10-485-225-88 Sequence 88, Appl
C 99 13 7.3 21 24 US-11-070-332-20 Sequence 20, Appl
C 100 13 7.3 21 24 US-11-070-332-21 Sequence 21, Appl
C 100 13 7.3 21 24 US-11-070-332-22 Sequence 22, Appl
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## ALIGNMENTS

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RESULT 1
US-10-719-900-631977/c
; Sequence 631977, Application US/10719900
; Publication No. US2005026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US/10/719,900
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 631977
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-631977

Query Match
Best Local Similarity 100.0%; Score 15; DB 21; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 25 AGGGGTGAGCGCCA 39
DB 21 AGGGGTGAGCGCCA 7

RESULT 2
US-10-719-956-616622/c
; Sequence 616622, Application US/10719956
; Publication No. US20040146910A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Rat
; FILE REFERENCE: 3527.1
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: US/10/719,956
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 699466
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 616622
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-719-956-616622
```

```
Query Match
Best Local Similarity 100.0%; Score 15; DB 22; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 18 CATGAGCAGGATGCTG 32
DB 17 CATGAGCAGGATGCTG 3
```

```
RESULT 3
US-11-036-317-231424/c
; Sequence 231424, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 231424
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-231424
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```
Query Match
Best Local Similarity 100.0%; Score 15; DB 24; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 149 TGAGTATGTGACTCT 163
DB 21 TGAGTATGTGACTCT 7
```

```
RESULT 4
US-11-036-317-267405/c
; Sequence 267405, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 267405
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-267405
```

```
Query Match
Best Local Similarity 100.0%; Score 15; DB 24; Length 25;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 149 TGAGTATGTGACTCT 163
DB 23 TGAGTATGTGACTCT 9
```

```
RESULT 5
US-11-036-317-357375/c
; Sequence 357375, Application US/11036317
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:25:05 ; Search time 54.6219 seconds  
(without alignments)  
5332.244 Million cell updates/sec

Title: US-09-887-941B-6

Perfect score: 178

Sequence: 1 gggccgtcgtcgaatgcat.....actctgcacccatttctcg 178

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818136359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database : Issued Patents, NA:\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PTCUTS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14	7.9	25	4	US-09-396-196G-21863
2	13	7.3	20	3	US-08-761-243C-1
3	13	7.3	20	2	US-08-444-818-775
4	13	7.3	21	2	US-08-403-888A-95
5	13	7.3	22	4	US-09-684-938-84
6	13	7.3	22	4	US-09-308-825A-84
7	13	7.3	25	4	US-09-396-196G-127035
8	13	7.3	28	2	US-08-761-243C-21
9	13	7.3	29	3	US-08-646-265A-55
10	13	7.3	31	4	US-09-615-095-6
11	13	7.3	33	4	US-08-407-620A-38
12	13	7.3	34	3	US-08-444-818-776
13	13	7.3	47	4	US-09-422-978-1672
14	12	6.7	15	2	US-08-292-620A-336
15	12	6.7	15	3	US-09-071-845-336
16	12	6.7	17	3	US-09-358-972-252
17	12	6.7	17	3	US-09-383-316-88
18	12	6.7	17	4	US-09-404-912-619
19	12	6.7	17	4	US-09-790-417-252
20	12	6.7	18	3	US-09-554-834A-6
21	12	6.7	19	3	US-09-277-078-19
22	12	6.7	19	3	US-09-091-952A-86
23	12	6.7	19	4	US-09-696-791-393
24	12	6.7	20	1	US-07-847-055A-3
25	12	6.7	20	3	US-09-395-604A-8
26	12	6.7	21	3	US-09-233-086-61
27	12	6.7	21	4	US-09-232-785-145

28	12	6.7	24	4	US-10-242-549-8	Sequence 8, Appli
29	12	6.7	24	4	US-10-242-549-10	Sequence 10, Appli
30	12	6.7	24	4	US-10-242-549-12	Sequence 12, Appli
31	12	6.7	24	4	US-10-242-549-14	Sequence 14, Appli
32	12	6.7	24	4	US-10-242-549-16	Sequence 16, Appli
33	12	6.7	24	4	US-10-242-549-18	Sequence 18, Appli
34	12	6.7	24	4	US-10-242-549-20	Sequence 20, Appli
35	12	6.7	24	4	US-10-242-549-22	Sequence 22, Appli
36	12	6.7	24	4	US-10-242-549-24	Sequence 24, Appli
37	12	6.7	25	3	US-09-641-259B-27	Sequence 27, Appli
38	12	6.7	25	4	US-08-062-021A-22	Sequence 22, Appli
39	12	6.7	25	4	US-09-396-196G-2387	Sequence 2387, Ap
40	12	6.7	25	4	US-09-396-196G-3001	Sequence 3001, Ap
41	12	6.7	25	4	US-09-396-196G-14159	Sequence 14159, A
42	12	6.7	25	4	US-09-396-196G-27794	Sequence 27794, A
43	12	6.7	25	4	US-09-396-196G-27795	Sequence 27795, A
44	12	6.7	25	4	US-09-396-196G-40486	Sequence 40486, A
45	12	6.7	25	4	US-09-396-196G-47361	Sequence 47361, A
46	12	6.7	25	4	US-09-396-196G-51506	Sequence 51506, A
47	12	6.7	25	4	US-09-396-196G-51507	Sequence 51507, A
48	12	6.7	25	4	US-09-396-196G-51508	Sequence 51508, A
49	12	6.7	25	4	US-09-396-196G-84577	Sequence 84577, A
50	12	6.7	25	4	US-09-396-196G-103218	Sequence 103218,
51	12	6.7	25	4	US-09-396-196G-108711	Sequence 108711,
52	12	6.7	25	4	US-09-396-196G-108712	Sequence 108712,
53	12	6.7	25	4	US-09-396-196G-108713	Sequence 108713,
54	12	6.7	25	4	US-09-396-196G-109647	Sequence 109647,
55	12	6.7	25	4	US-09-396-196G-127036	Sequence 127036,
56	12	6.7	28	3	US-08-613-822-8	Sequence 8, Appli
57	12	6.7	28	3	US-09-479-729B-8	Sequence 8, Appli
58	12	6.7	28	3	US-09-717-209-8	Sequence 8, Appli
59	12	6.7	31	1	US-08-136-993-19	Sequence 19, Appli
60	12	6.7	31	2	US-08-454-557C-63	Sequence 63, Appli
61	12	6.7	31	2	US-08-340-426D-63	Sequence 63, Appli
62	12	6.7	31	2	US-08-450-673C-63	Sequence 63, Appli
63	12	6.7	31	2	US-09-387-659-20	Sequence 20, Appli
64	12	6.7	31	3	US-09-641-259B-20	Sequence 20, Appli
65	12	6.7	31	5	PCT-US95-17111A-63	Sequence 63, Appli
66	12	6.7	32	4	US-09-153-447-16	Sequence 16, Appli
67	12	6.7	32	4	US-09-153-447-25	Sequence 25, Appli
68	12	6.7	32	4	US-09-721-908-54	Sequence 54, Appli
69	12	6.7	32	1	US-08-136-993-18	Sequence 18, Appli
70	12	6.7	35	1	US-09-066-597-14	Sequence 14, Appli
71	12	6.7	41	3	US-09-066-597-15	Sequence 15, Appli
72	12	6.7	42	3	US-09-109-063-24	Sequence 24, Appli
73	12	6.7	42	3	US-09-448-310-24	Sequence 24, Appli
74	12	6.7	42	4	US-09-884-948-24	Sequence 24, Appli
75	12	6.7	42	4	US-09-882-864A-23	Sequence 23, Appli
76	12	6.7	46	3	US-09-066-597-12	Sequence 12, Appli
77	12	6.7	47	3	US-09-641-638-671	Sequence 671, Appli
78	12	6.7	47	3	US-09-641-638-779	Sequence 779, Appli
79	12	6.7	47	4	US-09-422-978-1930	Sequence 3930, Ap
80	12	6.7	47	4	US-10-170-097-671	Sequence 671, Appli
81	12	6.7	47	4	US-10-170-097-671	Sequence 671, Appli
82	12	6.7	47	4	US-10-170-097-779	Sequence 779, Appli
83	12	6.7	49	4	US-09-424-378A-17	Sequence 17, Appli
84	12	6.7	50	2	US-08-540-804-35	Sequence 35, Appli
85	12	6.7	50	2	US-08-218-265-35	Sequence 35, Appli
86	12	6.7	50	3	US-08-521-872-35	Sequence 35, Appli
87	12	6.7	50	3	US-08-521-872-35	Sequence 35, Appli
88	12	6.7	50	3	US-08-521-872-35	Sequence 35, Appli
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96	12	6.7	50	4	US-10-242-549-29	Sequence 29, Appli
97	12	6.7	50	4	US-10-242-549-29	Sequence 29, Appli
98	12	6.7	50	4	US-10-242-549-29	Sequence 29, Appli
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100	12	6.7	50	4	US-10-242-549-29	Sequence 29, Appli

## ALIGNMENTS

RESULT 1  
US-09-396-196G-21863

Sequence 21863, Application US/09396196G

Patent No. 6821724

GENERAL INFORMATION:

APPLICANT: Michael Miltmann

APPLICANT: David Mack

APPLICANT: David Lockhart

APPLICANT: Affimetrix, Inc.

TITLE OF INVENTION: Methods of Genetic Analysis

FILE REFERENCE: 3101.1

CURRENT APPLICATION NUMBER: US/09/396,196G

CURRENT FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: 60/100,678

PRIOR FILING DATE: 1998-09-17

NUMBER OF SEQ ID NOS: 127806

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 21863

LENGTH: 25

TYPE: DNA

ORGANISM: Mus musculus

US-09-396-196G-21863

Query Match

Best Local Similarity 7.9%; Score 14; DB 4; Length 25;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 TTCACGAGGGAACC 90

DB 1 TTCACGAGGGAACC 14

RESULT 2

US-08-761-243C-1

Sequence 1, Application US/08761243C

Patent No. 5879879

GENERAL INFORMATION:

APPLICANT: Kamal D. Mehta

TITLE OF INVENTION: No. 5879879e1 Cis-Acting Element In The Human LDL Receptor Pro

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSSEE: Benjamin Aaron Adler, Ph.D., J.D.

STREET: 8011 Candle Lane

CITY: Houston

STATE: Texas

COUNTRY: USA

ZIP: 77071

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh

SOFTWARE: Microsoft Word for Macintosh

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/761,243C

FILING DATE: December 6, 1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Benjamin Aaron Adler, Ph.D., J.D.

REGISTRATION NUMBER: 35,423

REFERENCE/DOCKET NUMBER: D5956

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-777-2321

TELEFAX: 713-777-6908

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 bp

TYPE: nucleic acid

STRANDEDNESS: double-stranded

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: No

HYPOTHETICAL: No

ANTI-SENSE: NO

ORIGINAL SOURCE:

US-08-761-243C-1

Query Match

Best Local Similarity 7.3%; Score 13; DB 2; Length 20;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 TCACGGGTAAAA 66

DB 6 TCACGGGTAAAA 18

RESULT 3

US-08-444-818-775/C

Sequence 775, Application US/08444818

Patent No. 615087

GENERAL INFORMATION:

APPLICANT: Chien, David Y.

APPLICANT: Rutler, William J.

TITLE OF INVENTION: NANBV diagnostics and vaccines

NUMBER OF SEQUENCES: 777

CORRESPONDENCE ADDRESS:

ADDRESSSEE: Chiron Corporation

STREET: 4560 Horton Street

CITY: Emeryville

STATE: CA

COUNTRY: USA

ZIP: 94608-2916

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444,818

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/403,590

FILING DATE: 14-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hardin, Alisa A.

REGISTRATION NUMBER: 33,895

REFERENCE/DOCKET NUMBER: 0110.002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (508)359-3876

TELEFAX: (508)359-3885

INFORMATION FOR SEQ ID NO: 775:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "primer sscsh20A - derived

DESCRIPTION: from clone 5h"

US-08-444-818-775

Query Match

Best Local Similarity 7.3%; Score 13; DB 3; Length 20;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 157 TGACTGTGTCACC 169

DB 20 TGACTGTGTCACC 8

RESULT 4

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:22:30 : Search time 1238.07 Seconds  
(without alignments)  
5472.564 Million cell updates/sec

Title: US-09-887-941B-6

Perfect score: 178  
Sequence: 1 gggtcgcgtcgtgaatgatc.....actctgcaccattctctg 178

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hcc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsal:\*  
9: gb\_gsal2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	13	7.3	35	7	N36850 yv08e11.r1
4	13	7.3	40	8	AZ575761 AST-T3280
5	13	7.3	42	8	BH000535 2M0288B05
6	13	7.3	46	7	R24341 yv32h04.r1
7	13	7.3	46	7	R36760 yv22a04.r1
8	13	7.3	49	6	C20874 HUMG000494
9	13	7.3	50	1	AU104332 AU104337
10	13	7.3	31	1	AA615114 yv034h05.r
11	12	6.7	34	7	T89869 yd99e12.r1
12	12	6.7	34	8	AZ511608 1M0356A13
13	12	6.7	35	4	A1801185 t079h04.x
14	12	6.7	35	8	AZ658296 1M0535F04
15	12	6.7	36	7	R85453 yv26g04.r1
16	12	6.7	38	1	A1088003 co24h05.x
17	12	6.7	38	7	H45829 yv01b05.r1
18	12	6.7	38	9	BX658508 Arabidops
19	12	6.7	40	7	W96297 ze42a10.r1
20	12	6.7	41	1	AA019796 ze62h02.r
21	12	6.7	43	6	CB471442 sn3.A03
22	12	6.7	43	7	H59371 yv27h06.r1
23	12	6.7	43	7	R07988 yv16f09.r1
24	12	6.7	43	8	BH805136 1008065F0

25	12	6.7	43	9	BX651282 Arabidops
26	12	6.7	43	1	CL528416 ASV10D06
27	12	6.7	44	1	A1494250 qy98a01.x
28	12	6.7	45	7	N79952 yv28g01.r1
29	12	6.7	47	9	BX244624 Dario rer
30	12	6.7	48	8	AZ336853 1M0067K15
31	12	6.7	49	5	BQ587334 E012340W-
32	12	6.7	49	5	BQ587334 E012340W-
33	12	6.7	49	7	D11989 HUM0005134
34	12	6.7	50	1	AU102898 AU102898
35	12	6.7	50	1	AU106860 AU106860
36	12	6.7	50	1	AU106864 AU106864
37	12	6.7	50	1	AU106865 AU106865
38	12	6.7	50	8	AZ575772 AST-T3280
39	12	6.7	50	9	BX894616 Arabidops
40	12	6.2	20	9	AG195490 Pan trog1
41	12	6.2	22	9	AG201938 Pan trog1
42	12	6.2	24	8	AZ491197 1M0324C10
43	12	6.2	25	8	AZ486309 1M0314B18
44	12	6.2	25	8	AZ586862 1M0394A10
45	12	6.2	26	8	AZ307056 1M0008Q23
46	12	6.2	28	8	AZ806070 2M0067G21
47	12	6.2	29	8	AZ619274 1M0451J02
48	12	6.2	29	9	AG018559 Homo sapi
49	12	6.2	30	8	AZ408503 1M0179P12
50	12	6.2	30	8	AZ633504 1M0488K13
51	12	6.2	30	8	BZ352917 SALK_1194
52	12	6.2	31	4	BG503651 602549510
53	12	6.2	31	9	DR34P19S Dario rer
54	12	6.2	32	1	AJ666396 AJ666396
55	12	6.2	32	2	BE318502 NF071E02L
56	12	6.2	32	2	BE318791 NF075H02L
57	12	6.2	32	8	AZ946018 2M0207D07
58	12	6.2	34	1	AU014066 AU014066
59	12	6.2	34	1	AU248882 AU248882
60	12	6.2	34	7	U44145 ENU44145 As
61	12	6.2	34	9	AG201685 Pan trog1
62	12	6.2	35	8	AZ583415 1M0378024
63	12	6.2	35	8	AZ815423 2M0083H09
64	12	6.2	36	9	AJ594687 Arabidops
65	12	6.2	37	8	BZ770609 SALK_1435
66	12	6.2	37	8	CC057412 SALK_1417
67	12	6.2	38	2	BF507311 BFO507311 8949F-20
68	12	6.2	38	8	BZ287177 SALK_0205
69	12	6.2	38	9	CNS079KX AL060857 Amphelies
70	12	6.2	38	9	HSMC39C10 X88090 H.sapiens D
71	12	6.2	40	1	A1495995 sa94c05.y
72	12	6.2	40	9	AL950398 Arabidops
73	12	6.2	41	2	AM246496 2820488.3
74	12	6.2	41	8	AZ412970 1M0186G15
75	12	6.2	42	1	AA703076 2176h06.s
76	12	6.2	42	2	AV952678 AV952678
77	12	6.2	42	7	D19560 MUGS00962
78	12	6.2	43	1	AA625513 af72e05.r
79	12	6.2	43	7	R32204 yv85f06.r1
80	12	6.2	43	8	BZ289075 SALK_0224
81	12	6.2	44	2	AV958656 AV958656
82	12	6.2	44	8	AZ403273 1M0171G12
83	12	6.2	45	9	BX243596 Dario rer
84	12	6.2	46	9	AX2820550 2M0092M18
85	12	6.2	46	9	CL868623 EY14285-5
86	12	6.2	47	1	AV947917 AV947917
87	12	6.2	47	1	BU000922 BU000922
88	12	6.2	47	8	BZ597134 SALK_0994
89	12	6.2	48	2	AV958077 AV958077
90	12	6.2	48	9	TA197F02P AY447585 T. brucei
91	12	6.2	49	1	AM733869 AY947788
92	12	6.2	49	1	CC325445 TEA127 Ba
93	12	6.2	49	9	AG191198 Pan trog1
94	12	6.2	50	1	AU102624 AU102624
95	12	6.2	50	1	AU102625 AU102625
96	12	6.2	50	1	AU102626 AU102626
97	12	6.2	50	1	AU102626 AU102626



C 98	11	6.2	50	1	AU102674	AU102674
C 99	11	6.2	50	1	AU102677	AU102677
C 100	11	6.2	50	1	AU105599	AU105599

## ALIGNMENTS

[illegible]

LOCUS	25 bp	mrna	linear	EST 01-DEC-1995
DEFINITION	H030812.r1 Soares fetal liver spleen INLIS Homo sapiens cDNA clone			
IMAGE:	242182 5' similar to gb M87933 HMDAAU364 Human carcinoma cell-derived Alu RNA transcript, (rRNA), mRNA sequence.			
ACCESSION	U00532			

ACCESSION	H93534
VERSION	H93534.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens

REFERENCE  
AUTHORS  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M.,  
1 (bases 1 to 25)  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

TITLE	The Washu-Merck EST Project
JOURNAL	Unpublished (1995)
COMMENT	Contact: Wilson RK

```

Email: est@watson.wustl.edu
High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LINTL
This clone is available royalty-free through LINTL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Seq primer: MJ3RP1
High quality sequence stop: 1
Location/Qualifiers
1..25
FEATURES
source
```

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3791315"
/db_xref="taxon:9606"
/clone="IMAGE:242182"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/clone_id="Soares fetal liver spleen INFLs"
/note="Organ: Liver and Spleen; Vector: pT7/3D (Pharmacia)
with a modified polylinker; Site 1: Pac I; Site 2: Eco R.;
1st strand cDNA was primed with a Pac I - oligo(dT) primer
[5' AACTGACAGATTAATTAAAGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors:
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7/3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fátima Bonafide."

```

Query Match 7.3%; Score 13; DB 7; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 5,1e+04;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 159 ACTCTGTACCCCA 171  
 |||||  
 b 1 ACTCTGTACCCCA 13

RESULT 2	LOCUS	DEFINITION	LOCUS
BH758806/c	BH758806	33 bp DNA linear GSS 01-MAR-2002	
	SAUK_031345.51.20.x	Arabidopsis thaliana TDNA insertion lines	
	Arabidopsis thaliana genomic clone SAUK_031345.51.20.x	genomic	
	survey sequence.		
	BH758806		

ACCESSION	BH756806	
VERSION	BH756806.1	GI:19044689
KEYWORDS	GSS	
SOURCE	Arabidopsis thaliana (thale cress)	
ORGANISM	Arabidopsis thaliana	

REFERENCE  
AUTHORS  
Alonso, J.M., Leisse, T.U., Barajas, P., Chen, H., Cheuk, R.,  
1 (baes 1 to 33)  
Rosids; eucotsid II; Brassicales; Brassicaceae; Arabidopsis.

**TITLE** A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome  
**JOURNAL** Unpublished (2001)  
**COMMENT** Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGNAL)  
The Salk Institute for Biological Studies  
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA  
Tel: 858 453 4100 x1752  
Fax: 858 558 6379  
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of  
TDNA. This sequence lies within an annotated exon of At3g553700  
Class: TDNA tagged.

```

FEATURES
source
    Location/Qualifiers
        1..33
        /organism="Arabidopsis thaliana"
        /mol_type="Genomic DNA"
        /ecotype="Col-0"
        /db_xref="taxon:3702"
        /clone="SAUK_031145.51.20.x"
        /clone_11b="Arabidopsis thaliana TDNA insertion lines"
        /note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.sauk.edu/cdna\_protocols.html"

```

Query Match	7.3%	Score 13	DB 8	Length 33
Best Local Similarity	100.0%	Pred. No. 5.1e+04		
Matches 13	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	57	CGGGTTAAACC	69	
Db	27	CGGGTTAAACC	15	
RESULT 3				
N38850/c				
LOCUS				
DEFINITION				
N38850	35 bp	mRNA	linear	EST 19-JAN-1996
yy80ell.r1 Soares, multiple_sclerosis_2nbhmsp Homo sapiens cDNA				
clone IMAGE:279884 5' similar to gb M67933 HUMALU364 Human				
carcinoma cell-derived Alu RNA transcript. (rRNA) ; gb:M96956				
EPIDERMAL GROWTH FACTOR-LIKE CRIPTO PROTEIN (HUMAN) ; mRNA				
sequence.				
N38850				
N38850.1	GI:1162057			
VERSION				
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
	1 (bases 1 to 35)			
REFERENCE				

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 187.181 Seconds  
(without alignments)  
5629.394 Million cell updates/sec

Title: US-09-887-941B-6

Perfect score: 178  
Sequence: 1 99gtccgtcgtcgaatgcattttctg 178

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size: 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database: N\_Geneseq\_16Dec04:\*

1: geneeqn1980s:\*\n2: geneeqn1990s:\*\n3: geneeqn2000s:\*\n4: geneeqn2001as:\*\n5: geneeqn2001bs:\*\n6: geneeqn2002as:\*\n7: geneeqn2002bs:\*\n8: geneeqn2003as:\*\n9: geneeqn2003bs:\*\n10: geneeqn2003cs:\*\n11: geneeqn2003ds:\*\n12: geneeqn2004as:\*\n13: geneeqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15	8.4	35	3	AAC64260 Soybean c
C 2	14	7.9	20	12	AD115588 Human c
C 3	14	7.9	20	12	ADM34135 Human CD3
C 4	14	7.9	20	12	ADM11332 Human CD3
C 5	14	7.9	21	4	AAF93016 Wild type
C 6	14	7.9	25	9	ACT48004 Human m1c
C 7	14	7.9	25	9	ACK29975 Human m1c
C 8	14	7.9	26	10	ADCS4012 SAM4 PCR
C 9	14	7.9	41	6	AB244347 Human ATP
C 10	14	7.9	41	6	AB246696 Human ATP
C 11	14	7.9	42	2	AAT25575 Human gen
C 12	13	7.3	17	12	ADP09407 Extend pr
C 13	13	7.3	18	12	AD081024 Human pri
C 14	13	7.3	19	12	ADM6491 Human sho
C 15	13	7.3	19	12	ADP09402 Extend pr
C 16	13	7.3	19	12	ADP26951 Human P-C
C 17	13	7.3	20	8	AA118844 FPI enhan
C 18	13	7.3	20	8	ACC55324 Human ADA
C 19	13	7.3	20	12	ADH70943 Human Vde
C 20	13	7.3	20	13	ADT01088 Novel mut

C 21	13	7.3	21	2	AA061954 Human tYP
C 22	13	7.3	21	3	AAA89981 PCR prime
C 23	13	7.3	21	4	AA17802 Zea may
C 24	13	7.3	21	8	AB221583 Biliary g
C 25	13	7.3	21	9	ADB81017 RING-SH c
C 26	13	7.3	21	9	ADB81016 RING-SH c
C 27	13	7.3	21	9	ADB81018 RING-SH c
C 28	13	7.3	21	10	ADD19935 Oreochrom
C 29	13	7.3	21	10	AA156250 Human ubi
C 30	13	7.3	21	10	AA156249 Human ubi
C 31	13	7.3	21	10	AA156248 Human ubi
C 32	13	7.3	21	10	ADH73577 siRNA POS
C 33	13	7.3	21	13	ADH73575 siRNA POS
C 34	13	7.3	21	13	ADR89709 Human POS
C 35	13	7.3	21	13	ADR89710 Human POS
C 36	13	7.3	21	13	ADR89708 Human POS
C 37	13	7.3	21	13	ADS34641 POSH prot
C 38	13	7.3	21	13	ADS34640 POSH prot
C 39	13	7.3	21	13	ADS34642 POSH prot
C 40	13	7.3	22	8	ABX56408 Human NOV
C 41	13	7.3	22	10	ADH73576 siRNA POS
C 42	13	7.3	22	12	AD016814 4 synthet
C 43	13	7.3	24	4	AAH48127 Ribonucle
C 44	13	7.3	24	4	AA165251 Human diH
C 45	13	7.3	24	4	AAH75870 Human rev
C 46	13	7.3	24	5	AAH44468 Enolpyruv
C 47	13	7.3	24	5	AA168386 Human ATP
C 48	13	7.3	24	6	AA166326 Human thy
C 49	13	7.3	24	6	ABQ75907 Human L1
C 50	13	7.3	24	6	ABK86233 Arginyl t
C 51	13	7.3	25	9	ACT03920 Human m1c
C 52	13	7.3	25	9	ACT13157 Human m1c
C 53	13	7.3	25	9	ACK05705 Human m1c
C 54	13	7.3	25	9	ACT13180 Human m1c
C 55	13	7.3	25	9	ACT187917 Human m1c
C 56	13	7.3	25	9	ACT190803 Human m1c
C 57	13	7.3	25	9	ACK07676 Human m1c
C 58	13	7.3	25	9	ACK05340 Human m1c
C 59	13	7.3	25	9	ACT182151 Human m1c
C 60	13	7.3	26	12	ADP30756 Bacillus
C 61	13	7.3	28	2	AA118861 Human low
C 62	13	7.3	29	2	AAQ94508 Human/mur
C 63	13	7.3	29	2	AAT18622 Chimaeric
C 64	13	7.3	30	4	AA117808 Zea may
C 65	13	7.3	30	5	AB139683 Human cub
C 66	13	7.3	31	5	AA160078 Primer #2
C 67	13	7.3	33	6	ABA96568 Human tyr
C 68	13	7.3	33	6	ABA95478 Human diH
C 69	13	7.3	33	10	AA156444 Primer 3
C 70	13	7.3	37	10	ADG79070 Schizophr
C 71	13	7.3	39	2	AA60917 M. tuberc
C 72	13	7.3	39	3	AA27506 M13-tagge
C 73	13	7.3	41	6	ABA96570 Human tyr
C 74	13	7.3	41	6	ABA96571 Human tyr
C 75	13	7.3	41	6	ABN68870 Human mac
C 76	13	7.3	41	6	ABN68871 Human mac
C 77	13	7.3	41	6	AB247452 Human ATP
C 78	13	7.3	41	6	AB247556 Human ATP
C 79	13	7.3	41	6	AB247125 Human ATP
C 80	13	7.3	41	6	AB243249 Human ATP
C 81	13	7.3	41	6	ABA95480 Human diH
C 82	13	7.3	41	6	ABA95481 Human diH
C 83	13	7.3	41	10	AA156446 Probe 1 r
C 84	13	7.3	41	12	ADK17858 Cytochrom
C 85	13	7.3	47	3	AA267325 Human map
C 86	13	7.3	47	3	AA267326 Human map
C 87	13	7.3	47	13	ADR35380 Human n1c
C 88	13	7.3	47	13	ADR35379 Human n1c
C 89	13	7.3	47	13	ADR35398 Human n1c
C 90	13	7.3	47	13	ADR35399 Human n1c
C 91	13	7.3	49	8	AB209708 Human oli
C 92	13	7.3	49	10	AB279161 Tumour su
C 93	13	6.7	50	6	AB207763 Human leu
C 94	13	6.7	51	5	ABF99107 Oligonuc

```
c 94 12 6.7 13 5 ABC96633 Abc96633 Oligonuc
95 12 6.7 13 5 ABP99106 Abf99106 Oligonuc
96 12 6.7 13 5 ABC96632 Abc96632 Oligonuc
97 12 6.7 14 8 Aca61142 Aca61142 Adaptein
98 12 6.7 15 2 Aat52086 Aat52086 Human ICA
99 12 6.7 17 3 Aaa36560 Aaa36560 Human gen
c 100 12 6.7 17 3 Aaa87041 Aaa87041 Probe to
```

## ALIGNMENTS

## RESULT 1

```
AAc64260/c
ID AAC64260 standard; DNA; 35 BP.
```

```
XX AAC64260;
```

```
DT 23-FEB-2001 (first entry)
```

```
DE Soybean cotyledon leucine aminopeptidase (LAP) PCR primer, SEQ ID NO:9.
```

```
KW Soybean cotyledon; leucine aminopeptidase; LAP; recombinant production;
```

```
KM plasmid construction; PCR primer; ss.
```

```
XX Glycine max.
```

```
PN JP2000262286-A.
```

```
PD 26-SEP-2000.
```

```
PF 15-MAR-1999; 99JP-00068353.
```

```
PR 15-MAR-1999; 99JP-00068353.
```

```
XX (AJIN ) AJINOMOTO KK.
```

```
DR WPI; 2000-682117/67.
```

```
PT Novel DNA encoding leucine aminopeptidase useful for the recombinant
```

```
PT preparation of leucine aminopeptidase.
```

```
XX Example 3; Page 20; 22pp; Japanese.
```

```
CC The invention relates to a soybean leucine aminopeptidase (AAB29636), and
```

```
CC cDNA encoding it (AAC64260), derived from cotyledon tissue. The invention
```

```
CC also relates to variants of soybean cotyledon LAP which retain activity,
```

```
CC recombinant vectors and host cells comprising DNA encoding the soybean
```

```
CC cotyledon LAP, and a method for the recombinant production of the LAP.
```

```
CC The method of the invention can be used for the large scale recombinant
```

```
CC preparation of soybean cotyledon leucine aminopeptidase. The present
```

```
CC sequence represents a soybean cotyledon leucine aminopeptidase PCR primer
```

```
CC used in plasmid construction in an exemplification of the invention
```

```
XX SQ Sequence 35 BP; 7 A; 8 C; 10 G; 10 T; 0 U; 0 Other;
```

```
OY 90 CACGTGCCATTTTAA 104
```

```
DB 21 CACGTGCCATTTTAA 7
```

```
XX ADI15588/c
```

```
XX ADI15588; standard; DNA; 20 BP.
```

```
XX ADI15588;
```

```
XX 22-APR-2004 (first entry)
```

```
DE Human phosphodiesterase 4D antisense oligonucleotide #14.
```

```
KX cytosstatic; cardiant; antiinflammatory; antimicrobial; antisense therapy;
```

```
KW phosphodiesterase inhibitor 4D; phosphodiesterase 4D; cancer;
```

```
KM cardiovascular disease; inflammation; infection; inflammation;
```

```
XX tumour formation; antisense technology; human; ss.
```

```
OS Homo sapiens.
```

```
XX Key
```

```
FT modified_base
```

```
FT 1..20
```

```
FT /*tag= b
```

```
FT /mod_base= OTHER
```

```
FT /note= "OTHER= Phosphorothioate backbone. All cytidines
```

```
FT are 5-methylcytidines"
```

```
FT 1..5
```

```
FT /*tag= a
```

```
FT /mod_base= OTHER
```

```
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
```

```
FT 15..20
```

```
FT /*tag= c
```

```
FT /mod_base= OTHER
```

```
FT /note= "OTHER= 2'-O-Methoxyethyl (2'-MOE) nucleotides"
```

```
XX US2003220273-A1.
```

```
XX 27-NOV-2003.
```

```
XX 15-MAY-2002; 2002US-00146860.
```

```
XX 15-MAY-2002; 2002US-00146860.
```

```
XX (ISIS-) ISIS PHARM INC.
```

```
XX Bennett CF, Dobie KW, Roach MP;
```

```
XX WPI; 2004-060214/06.
```

```
XX New antisense compounds targeted to nucleic acid molecules encoding
```

```
XX phosphodiesterase 4D, useful for treating diseases associated with
```

```
XX expression of phosphodiesterase 4D, e.g. cancer, cardiovascular disease
```

```
XX or inflammation.
```

```
XX Example 15; SEQ ID NO 34; 72pp; English.
```

```
XX The invention describes a compound 8-80 nucleobases in length targeted to
```

```
XX a nucleic acid molecule encoding phosphodiesterase 4D. The compound
```

```
XX specifically hybridises with the nucleic acid molecule encoding
```

```
XX phosphodiesterase 4D and inhibits the expression of phosphodiesterase 4D,
```

```
XX or specifically hybridises with at least an 8-nucleobase portion of an
```

```
XX active site on a nucleic acid molecule encoding phosphodiesterase 4D. The
```

```
XX antisense oligonucleotides and compounds are useful for modulating the
```

```
XX expression of phosphodiesterase 4D, and for treating diseases or
```

```
XX conditions associated with expression of phosphodiesterase 4D, e.g.
```

```
XX cancer, cardiovascular disease or inflammation. The antisense compounds
```

```
XX are also useful as research reagents and kits, or in diagnostic,
```

```
XX therapeutic and prophylaxis applications, e.g. to prevent or delay
```

```
XX infection, inflammation or tumour formation. This sequence represents a
```

```
XX human phosphodiesterase 4D antisense oligonucleotide.
```

```
XX SQ Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
```

```
OY 81 CGAGGGAACACAGT 94
```

```
DB 15 CGAGGGAACACAGT 2
```

```
XX CGAGGGAACACAGT 94
```

```
XX 15 CGAGGGAACACAGT 2
```

```
XX 7.9%; Score 14; DB 12; Length 20;
```

```
XX Best Local Similarity 100.0%; Pred. No. 2.5e+03;
```

```
XX Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
XX RESULT 3
```

```
XX ADM34135/c
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 1092.17 seconds  
(without alignments)  
7897.122 Million cell updates/sec

Title: US-09-887-941B-6  
Sequence: 1 gggtcgcgtcgtgatgcac.....actctgcaccacatttcctg 178

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size: 0  
Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database:

GenBml: 1: gb\_ba: \*  
2: gb\_hlg: \*  
3: gb\_in: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pl: \*  
9: gb\_pr: \*  
10: gb\_ro: \*  
11: gb\_sts: \*  
12: gb\_sy: \*  
13: gb\_un: \*  
14: gb\_vi: \*

Pred. NO. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	* Match	Length	DB ID	Description
C 1	14	7.9	21	6	AX092775
C 2	13	7.3	18	6	CQ788001 Sequence
C 3	13	7.3	19	6	CQ824199 Sequence
C 4	13	7.3	20	6	AR118841 Sequence
C 5	13	7.3	20	6	IO6413
C 6	13	7.3	20	12	AB069586
C 7	13	7.3	21	6	AR074287
C 8	13	7.3	21	6	BD182298
C 9	13	7.3	21	6	BD243279
C 10	13	7.3	21	6	AX032649
C 11	13	7.3	21	6	AX235821
C 12	13	7.3	21	6	AX776610
C 13	13	7.3	21	6	AX776612
C 14	13	7.3	22	6	AX804402
C 15	13	7.3	22	6	AR308944
C 16	13	7.3	22	6	AR317075
C 17	13	7.3	22	6	AX776611
C 18	13	7.3	26	6	AX951882
C 19	13	7.3	29	6	AX253564

C 20	13	7.3	30	6	BD187806	BD187806 Novel pol
C 21	13	7.3	30	6	AX235827	AX235827 Sequence
C 22	13	7.3	30	6	BD105529	BD105529 Novel pol
C 23	13	7.3	31	6	AR448492	AR448492 Sequence
C 24	13	7.3	31	6	AX078478	AX078478 Sequence
C 25	13	7.3	31	6	AX08601	AX08601 Oligonucleo
C 26	13	7.3	33	6	AR337935	AR337935 Sequence
C 27	13	7.3	34	6	AR118842	AR118842 Sequence
C 28	13	7.3	34	6	IO6414	IO6414 Sequence 34
C 29	13	7.3	39	6	AX022689	AX022689 Sequence
C 30	13	7.3	41	6	AX513835	AX513835 Sequence
C 31	13	7.3	41	6	AX517711	AX517711 Sequence
C 32	13	7.3	41	6	AX518142	AX518142 Sequence
C 33	13	7.3	47	6	AR289937	AR289937 Sequence
C 34	13	7.3	49	6	AX523198	AX523198 Sequence
C 35	12	6.7	15	6	AR056132	AR056132 Sequence
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C 44	12	6.7	18	6	AR367785	AR367785 Sequence
C 45	12	6.7	19	6	AX731669	AX731669 Sequence
C 46	12	6.7	19	6	AX709267	AX709267 Sequence
C 47	12	6.7	19	6	AX226153	AX226153 Sequence
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C 88	12	6.7	31	6	AR073178	AR073178 Sequence
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94 12 6.7 32 6 AR390458 Sequence  
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96 12 6.7 32 6 AR478854 Sequence  
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C 100 12 6.7 40 6 AX099972 Sequence

## ALIGNMENTS

RESULT 1  
AX092775/c  
LOCUS AX092775 21 bp DNA linear PAT 21-MAR-2001  
DEFINITION Sequence 187 from Patent WO0115676.  
ACCESSION AX092775 GI:13444832  
VERSION AX092775.1 GI:13444832  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Butleria; Primates; Catarrhini; Homnidae; Homo.  
TITLE Hayden, M.R., Brooks-Wilson, A.R., Pimstone, S.N. and Clee, S.M.  
JOURNAL Compositions and methods for modulating hdl cholesterol and  
PATENT: WO 0115676-A 187 08-MAR-2001;  
UNIVERSITY OF BRITISH COLUMBIA (CA); Xenon Genetics Inc. (CA)  
FEATURES  
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## ORIGIN

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QY 61 TTTAAACCCGACCA 74  
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17 TTTAAACCCGACCA 4

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LOCUS CQ788001/c 18 bp DNA linear PAT 24-MAR-2004  
DEFINITION Sequence 307 from Patent WO2004020664.  
ACCESSION CQ788001  
VERSION CQ788001.1 GI:45722959  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE  
1 Geldermann, H., Preuss, S. and Han, Y.  
AUTHORS Polymorphous microsatellite loci in genes for pre-diagnostic  
TITLE purposes  
JOURNAL Patent: WO 2004020664-A 307 11-MAR-2004;  
UNIVERSITÄT HOHENHEIM (DE)  
FEATURES  
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1. 18  
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16 ACTCTGTACCCA 4

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LOCUS CQ824199 19 bp DNA linear PAT 21-JUN-2004  
DEFINITION Sequence 52 from Patent EP1428893.  
ACCESSION CQ824199  
VERSION CQ824199.1 GI:49021151  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE  
1 Sprecher, E. and Bergman, R.  
AUTHORS Methods of and compositions for modulating hair growth via  
TITLE p-cadherin modulators  
JOURNAL Patent: EP 1428893-A 52 16-JUN-2004;  
FEATURES  
source  
1. 19  
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## ORIGIN

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QY 159 ACTCTGTACCCA 171  
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14 ACTCTGTACCCA 2

## RESULT 4

LOCUS AR118841/c 20 bp DNA linear PAT 16-MAY-2001  
DEFINITION Sequence 775 from patent US 6150087.  
ACCESSION AR118841  
VERSION AR118841.1 GI:14100751  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE  
1 Unclassified.  
AUTHORS Chien, D.Y.  
TITLE NABV diagnostics and vaccines  
JOURNAL Patent: US 6150087-A 775 21-NOV-2000;  
FEATURES  
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## ORIGIN

Query Match 7.3%; Score 13; DB 6; Length 20;  
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QY 157 TGACTCTGTACCC 169  
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20 TGACTCTGTACCC 8

RESULT 5  
LOCUS 106413/c 20 bp DNA linear PAT 02-DEC-1994  
DEFINITION Sequence 33 from Patent EP 0318216.  
ACCESSION 106413

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 04:55:56 ; Search time 589.607 Seconds  
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Pred. No. is the number of results predicted by chance to have a  
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C 5	16	4.2	25	21	US-10-809-189-25049
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C 22	15	3.9	25	21	US-10-719-900-717793	Sequence 717793,
C 23	15	3.9	25	21	US-10-719-900-873588	Sequence 873588,
C 24	15	3.9	25	21	US-10-719-900-978474	Sequence 978474,
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C 29	15	3.9	25	21	US-10-956-157-40208	Sequence 40208, A
C 30	15	3.9	25	21	US-10-956-157-413285	Sequence 143285,
C 31	15	3.9	25	21	US-10-956-157-263877	Sequence 263877,
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c 96 14 3.6 25 21 US-10-956-157-173490, Sequence 173490,
c 97 14 3.6 25 21 US-10-956-157-271920, Sequence 271920,
c 98 14 3.6 25 22 US-10-843-527-60965, Sequence 60965, A
c 99 14 3.6 25 22 US-10-843-527-177212, Sequence 177212,
c 100 14 3.6 25 22 US-10-719-956-13264, Sequence 13264, A
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## ALIGNMENTS

## RESULT 1

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US-10-239-734-20/c
; Sequence 20, Application US/10239734
; Publication No. US20040161746A1
; GENERAL INFORMATION:
; APPLICANT: GENOX RESEARCH, INC.
; APPLICANT: JAPAN AS REPRESENTED BY GENERAL DIRECTOR OF AGENCY OF NATIONAL CENTER FOR
; APPLICANT: CHILD HEALTH AND DEVELOPMENT
; APPLICANT: Matsumoto, Yoshiko
; APPLICANT: Tsujimoto, Goshoh
; APPLICANT: Nagasu, Takeshi
; APPLICANT: Sugita, Yuji
; APPLICANT: Oshida, Tadahiro
; APPLICANT: Imai, Yukiko
; TITLE OF INVENTION: Method of Testing For Allergic Disease
; FILE REFERENCE: SHIMIZU-07379
; CURRENT APPLICATION NUMBER: US/10/239,734
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/JP01/11286
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 2000-389476 JP
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: an artificially synthesized Tagman probe sequence
; NAME/KEY: misc binding
; LOCATION: (1)..(1)
; OTHER INFORMATION: Label FAM (6-carboxy-fluorescein)
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; NAME/KEY: misc binding
; LOCATION: (28)..(28)
; OTHER INFORMATION: Label TAMRA (6-carboxy-N,N,N',N'-tetramethylrhodamine)
US-10-239-734-20
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Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 218 GAGCTCTATGCGACCAAGA 237
Db 23 GACTCTATGCGACCAAGA 4
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US-11-036-317-846886/c
; Sequence 846886, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 846886
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-846886
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 25 AGGCCGAGTCTGCGGC 9
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US-10-719-900-106967/c
; Sequence 106967, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 106967
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-719-900-106967
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Query Match 4.2%; Score 16; DB 21; Length 25;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 50 TTCAATTCCTGGAGCC 65
Db 23 TTCAATTCCTGGAGCC 8
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RESULT 4
US-10-719-900-362302/c
; Sequence 362302, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
; PRIOR FILING DATE: 2002-11-20
; NUMBER OF SEQ ID NOS: 982914
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:25:05 ; Search time 117.836 Seconds  
(without alignments)  
5332.244 Million cell updates/sec

Title: US-09-887-941B-5

Perfect score: 384  
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Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 81813359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database : Issued Patents, NA:\*

- 1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*
- 2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*
- 3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*
- 4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*
- 5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*
- 6: /cgn2\_6/ptodata/1/ina/Backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	14	3.6	23	2	US-08-859-998-87
6	14	3.6	23	4	US-09-225-928-87
7	14	3.6	23	4	US-09-225-201B-87
8	14	3.6	25	4	US-09-396-196G-2879
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12	14	3.6	42	1	US-08-256-964A-6
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18	13	3.4	18	3	US-09-166-186-170
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33	13	3.4	20	3	US-09-166-186-153	Sequence 153, App
34	13	3.4	20	3	US-09-313-932-146	Sequence 146, App
35	13	3.4	20	3	US-09-313-932-147	Sequence 147, App
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38	13	3.4	20	3	US-09-313-932-150	Sequence 150, App
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46	13	3.4	22	1	US-08-287-075-7	Sequence 7, Appl
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48	13	3.4	22	3	US-07-974-409C-312	Sequence 312, App
49	13	3.4	22	4	US-09-269-446D-102	Sequence 102, App
50	13	3.4	22	5	PCT-US93-00977-11	Sequence 11, Appl
51	13	3.4	22	5	PCT-US93-00977-312	Sequence 312, App
52	13	3.4	24	4	US-09-093-972C-970	Sequence 970, App
53	13	3.4	25	4	US-09-396-196G-21198	Sequence 21198, A
54	13	3.4	25	4	US-09-396-196G-21199	Sequence 21199, A
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99	13	3.4	25	4	US-09-396-196G-125015	Sequence 125015, A
100	13	3.4	25	4	US-09-396-196G-125016	Sequence 125016, A



## ALIGNMENTS

## RESULT 1

US-09-396-196G-29049  
Sequence 29049, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Mack  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for windows Version 4.0  
SEQ ID NO 29049  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-09-396-196G-29049

Query Match 4.2%; Score 16; DB 4; Length 25;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 346 TGTGTGCCACAGATG 361  
DB 3 TGTGTGCCACAGATG 18

## RESULT 2

US-09-513-999C-15047/C  
Sequence 15047, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59, US2, REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 15047  
LENGTH: 50  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-513-999C-15047

Query Match 3.9%; Score 15; DB 4; Length 50;  
Best Local Similarity 100.0%; Pred. No. 6.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 87 TTTCCTGCCCCACA 101  
DB 29 TTTCCTGCCCCACA 15

## RESULT 3

US-09-289-368-69/C  
Sequence 69, Application US/09289368  
Patent No. 5998148

## GENERAL INFORMATION:

APPLICANT: C. Frank Bennett  
APPLICANT: Elizabeth J. Ackermann  
TITLE OF INVENTION: ANTISENSE MODULATION OF MICROTUBULE-ASSOCIATED PROTEIN 4 EXPRESSIC  
FILE REFERENCE: RTS-0051  
CURRENT APPLICATION NUMBER: US/09/289,368  
CURRENT FILING DATE: 1999-04-08  
NUMBER OF SEQ ID NOS: 87  
SEQ ID NO 69  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-289-368-69

Query Match 3.6%; Score 14; DB 2; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.1e+03;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 90 CCTGCCCCACACC 103  
DB 18 CCTGCCCCACACC 5

## RESULT 4

US-09-311-260-147  
Sequence 147, Application US/09311260  
Patent No. 6214555  
GENERAL INFORMATION:  
APPLICANT: Leusner, James  
APPLICANT: Hui, May  
APPLICANT: Dunn, James M.  
APPLICANT: Lacroix, Jean-Michel  
TITLE OF INVENTION: METHOD, COMPOSITIONS AND KIT FOR DETECTION OF  
TITLE OF INVENTION: MICROORGANISMS AND BI-DIRECTIONAL SEQUENCING OF NUCLEIC ACID  
NUMBER OF SEQUENCES: 189  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Opedahl & Larson LLP  
STREET: P.O. Box 5270  
CITY: Prisco  
STATE: CO  
COUNTRY: US  
ZIP: 80443-5270  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/311,260  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Larson, Marina T.  
REGISTRATION NUMBER: 32,038  
REFERENCE/DOCKET NUMBER: VGEN-P-058-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (970) 668-2050  
TELEFAX: (970) 668-2082  
TELEX:  
INFORMATION FOR SEQ ID NO: 147:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 21  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: no

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:22:30 ; Search time 2670.9 Seconds  
(without alignments)  
5472.564 Million cell updates/sec

Title: US-09-887-941B-5

Perfect score: 384  
Sequence: 1 caggccgcgcgagactccac.....atgagtgctgggaccgagcgt 384

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size: 0

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database:

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6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 4	14	3.6	47	8 B2381951	B2381951 SALK_1176
C 5	14	3.6	50	1 AUI06633	AUI06633 AUI06633
C 6	13	3.4	28	9 A2308339	A2308339 IM0011A18
C 7	13	3.4	28	9 AG265512	AG265512 locus cor
C 8	13	3.4	35	5 B0594628	B0594628 E012404-0
C 9	13	3.4	37	1 A1192854	A1192854 zp94a05.8
C 10	13	3.4	38	1 AUI257194	AUI257194 AUI257194
C 11	13	3.4	40	1 A0654389	A0654389 nt62d05.8
C 12	13	3.4	40	1 A0257305	A0257305 A0257305
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C 14	13	3.4	41	8 BH796123	BH796123 1008092H0
C 15	13	3.4	41	9 A0801895	A0801895 Drosophila
C 16	13	3.4	42	8 A2770413	A2770413 IM0572B01
C 17	13	3.4	42	8 BK244387	BK244387 Dario rer
C 18	13	3.4	44	9 BX001979	BX001979 Arabidops
C 19	13	3.4	45	8 A2809363	A2809363 2M0073014
C 20	13	3.4	47	9 AG204311	AG204311 Pan trogl
C 21	13	3.4	48	8 B2357549	B2357549 SALK_1308
C 22	13	3.4	49	9 CUS18625	CUS18625 DAE7B03.F
C 23	12	3.1	21	1 A0668099	A0668099 A0668099
C 24	12	3.1	21	8 A2991096	A2991096 2M0275C09

C 25	12	3.1	23	9	AG202483	AG202483 Pan trogl1
C 26	12	3.1	25	8	A2782142	A2782142 2M0022H10
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C 35	12	3.1	38	4	B1687189	B1687189 603307847
C 36	12	3.1	38	8	A2657875	A2657875 1M0534A19
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C 41	12	3.1	41	8	B2291498	B2291498 SALK_1208
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C 43	12	3.1	42	1	AL588371	AL588371 AL588371
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C 45	12	3.1	42	9	CL459321	CL459321 AG0457.Sa
C 46	12	3.1	44	2	BE882963	BE882963 601505866
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C 78	11	2.9	25	8	AZ776639	AZ776639 2M0010L02
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C 80	11	2.9	27	8	AZ404479	AZ404479 1M0172F18
C 81	11	2.9	27	1	AZ779701	AZ779701 2M0016M22
C 82	11	2.9	28	1	AA960907	AA960907 on92c04.s
C 83	11	2.9	28	8	AZ466703	AZ466703 1M0277N05
C 84	11	2.9	28	8	AZ605911	AZ605911 1M0427H01
C 85	11	2.9	28	8	AZ632301	AZ632301 1M0486C23
C 86	11	2.9	29	1	AL045592	AL045592 DKF2P343N
C 87	11	2.9	29	1	AZ331636	AZ331636 1M0059O09
C 88	11	2.9	29	8	AZ335953	AZ335953 1M0066O05
C 89	11	2.9	29	8	AZ822977	AZ822977 2M0096C09
C 90	11	2.9	29	8	AZ847949	AZ847949 2M0148B23
C 91	11	2.9	29	8	BH864803	BH864803 SALK_0968
C 92	11	2.9	29	8	CC457201	CC457201 SALK_1072
C 93	11	2.9	30	1	AL045336	AL045336 DKF2P434A
C 94	11	2.9	30	1	AL045352	AL045352 DKF2P434B
C 95	11	2.9	30	1	AL045477	AL045477 DKF2P434H
C 96	11	2.9	30	1	AL045487	AL045487 DKF2P434I
C 97	11	2.9	30	4	BM398771	BM398771 5009-0-5-

98 11 2.9 30 7 CK151329  
99 11 2.9 30 8 AZ211581  
c 100 11 2.9 31 1 AA793867

CK151329 GS1-128 S  
AZ211581 1M0027005  
AA793867 at46a11.s

## ALIGNMENTS

RESULT 1  
LOCUS W70854/c  
DEFINITION W70854 34 bp mRNA linear EST 17-JUN-1996  
md91f05.r1 Soares mouse embryo NDME13.5 14.5 Mus musculus cDNA  
clone IMAGE:385377 5' similar to SW:HCDD.PIG P00348  
3-HYDROXYACYL-CoA DEHYDROGENASE ; mRNA sequence.

ACCESSION W70854  
VERSION W70854.1 GI:1381006  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 34)  
AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,  
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,  
Schellenberg, K., Stepcoe, M., Tan, F., Underwood, K., Moore, B.,  
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and  
Waterston, R.

TITLE The WashU-HMI Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT Contact: Marra M/Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watsn.musl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
MG1:237209

Trace considered overall poor quality  
Possible reversed clone: similarity on wrong strand  
Seq primer: mob.REGA+ET  
High quality sequence stop: 1.  
Location/Qualifiers  
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/lab\_host="DH10B"  
/clone\_lib="Soares mouse embryo NDME13.5 14.5"  
/note="Vector: pRTT3D-Pac (Pharmacia) with a modified  
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA  
was primed with a Not I - oligo(dT) primer [5',  
TGTTACCAATCTGAAGTCGAGCGCCGCGAATTTTCTTTTCTTTTCTTTT  
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2  
14.5dpc embryos (total RNA provided by Minoru Ko, Wayne  
State Univ., from 2 1); double-stranded cDNA was ligated to  
Eco RI adaptors (Pharmacia), digested with Not I and  
cloned into the Not I and Eco RI sites of the modified  
pRTT3 vector. Library went through one round of  
normalization, and was constructed by Bento Soares and  
M.Fatima Bonaldo."

## ORIGIN

Query Match 3.6%; Score 14; DB 7; Length 34;  
Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 225 TATGCACCAAGAG 238  
DB 18 TATGCACCAAGAG 5

RESULT 2  
LOCUS AZ794093/c  
DEFINITION AZ794093 36 bp DNA linear GSS 16-FEB-2001  
2M0047012R Mouse 10kb plasmid UNGC1M library Mus musculus genomic  
clone UNGC2M0047012 R, genomic survey sequence.

ACCESSION AZ794093  
VERSION AZ794093.1 GI:12939709  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 36)  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
Niederhausen, A. and Wright, D. Weis, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weis  
University of Utah Genome Center  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert length: 10000 Spd Error: 0.00  
Plate: 0047 row: O column: 12  
Seq primer: CACACAGGAACGCTATGACC  
Class: Plasmid ends  
High quality sequence stop: 36.  
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/clone\_lib="Mouse 10kb plasmid UNGC1M library"  
/note="Vector: FMD42nv; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (G14732114|g|AP129072.11), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## FEATURES

source  
1..36  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (G14732114|g|AP129072.11), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 3.6%; Score 14; DB 8; Length 36;  
Best Local Similarity 100.0%; Pred. No. 3.9e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 403.806 Seconds  
(without alignments)  
5629.394 Million cell updates/sec

Title: US-09-887-941B-5  
Perfect score: 384  
Sequence: 1 cagagccgcgcgagaccac.....atgagctgtgagaccgcgcgt 384

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

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7: geneseq2002bs:\*  
8: geneseq2003as:\*  
9: geneseq2003bs:\*  
10: geneseq2003cs:\*  
11: geneseq2003ds:\*  
12: geneseq2004as:\*  
13: geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	15	3.9	19	AD045586	AD045586 Human oli
6	15	3.9	22	AAV51970	AAV51970 Zea may8
7	15	3.9	25	ACK17372	ACK17372 Human mic
8	15	3.9	25	ACK02627	ACK02627 Human mic
9	15	3.9	25	ACI56494	ACI56494 Human mic
10	15	3.9	25	ACI15356	ACI15356 Human mic
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12	15	3.9	25	ACI14985	ACI14985 Human mic
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14	15	3.9	40	AAV51134	AAV51134 Maize pol
15	15	3.9	42	AAV71123	AAV71123 Molecular
16	15	3.9	42	AAV71114	AAV71114 Molecular
17	15	3.9	42	AAV71119	AAV71119 Molecular
18	15	3.9	42	AAV71131	AAV71131 Molecular
19	15	3.9	42	AAV71127	AAV71127 Molecular
20	15	3.9	45	AAV70824	AAV70824 Molecular

C	21	15	3.9	46	3	AAV71094	AAV71094 Molecular
C	22	15	3.9	46	3	AAV71110	AAV71110 Molecular
C	23	15	3.9	46	3	AAV71087	AAV71087 Molecular
C	24	15	3.9	46	3	AAV71096	AAV71096 Molecular
C	25	15	3.9	46	3	AAV71099	AAV71099 Molecular
C	26	15	3.9	46	3	AAV71100	AAV71100 Molecular
C	27	15	3.9	46	3	AAV71104	AAV71104 Molecular
C	28	15	3.9	50	3	AAV71092	AAV71092 Human sec
C	29	14	3.6	17	3	AAV70623	AAV70623 Hammerhea
C	30	14	3.6	17	12	AD183762	AD183762 HCV DNAzy
C	31	14	3.6	20	3	AAZ88534	AAZ88534 Human mic
C	32	14	3.6	20	12	ADK96106	ADK96106 Primer of
C	33	14	3.6	20	12	ADK93583	ADK93583 Human MAD
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## ALIGNMENTS

## RESULT 1

ADQ30502  
 ID ADQ30502 standard; DNA; 22 BP.

AC ADQ30502;

DT 29-JUL-2004 (first entry)

DE Human novel GPCR PGR10 RT-PCR primer, SEQ ID NO:1605.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 KM transgenic mouse; neurological disorder; adrenal gland disorder;  
 KM colon disorder; intestinal disorder; cardiovascular disorder;  
 KM muscular disorder; blood disorder; immune disorder; bone disorder;  
 KM joint disorder; metabolic disorder; lung disorder; breast disorder;  
 KM kidney disorder; liver disorder; prostate disorder; testis disorder;  
 KM ovary disorder; uterus disorder; pancreas disorder; spleen disorder;  
 KM skin disorder; stomach disorder; thyroid disorder; antiparkinsonian; antianemic;  
 KM thymus disorder; thyroid disorder; vasotropic; antidiabetic;  
 KM cytoskeletal; antiinflammatory; vasotropic; antidiabetic; antidiabetic;  
 KM CNS; central nervous system; respiratory; antidiabetic; antidiabetic;  
 KM virucide; hepatotropic; antibacterial; antianemic; antiseborrheic;  
 KM dermatological; antitumor; antitumor; antitumor; antitumor;  
 KM immunosuppressive; nephrotropic; gene therapy; GPCR modulator; human;  
 KM PGR10; reverse transcription-PCR; RT-PCR; primer; ss.

OS Homo sapiens.

XX WO2004040000-A2.

PN 13-MAY-2004.

PD 09-SEP-2003; 2003WO-US028226.

PF 09-SEP-2002; 2002US-0409303P.

PR 09-APR-2003; 2003US-0461329P.

XX (PRIM-) PRIMML INC.

PA Gaitanaris GA, Bergmann JB, Gragerov A, Hohmann U, Li F,  
 PI Medisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;  
 XX WPI; 2004-3390329/36.

DR WPI; 2004-3390329/36.

XX Novel mammalian G protein coupled receptors, useful for identifying  
 PT compounds that modulates diagnosing and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 PT pectoris, Parkinson's disease.

PS Disclosure; SEQ ID NO 1605; 542bp; English.

XX The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; methods of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising

CC probes which hybridize to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease),  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia),  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders (e.g., autoimmune disorders or  
 CC anaemia or leukaemia); immune disorders (e.g., osteoarthritis, rheumatoid  
 CC AIDS); bone and joint disorders (e.g., osteoporosis); metabolic or  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a PCR primer  
 CC used in the isolation of cDNA encoding the novel human GPCR PGR10. Note:  
 CC The full sequence data for this patent did not form part of the printed  
 CC specification; those sequences not shown were obtained in electronic  
 CC format directly from WIPO at fcp.wipo.int/pub/published\_pcr\_sequences.

XX Sequence 22 BP; 5 A; 5 C; 8 G; 4 T; 0 U; 0 Other;

QY Query Match 5.7%; Score 22; DB 12; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.56;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 208 AGAACCGGCGGACTCTCTATGG 229

Db 1 AGAACCGGCGGACTCTCTATGG 22

AA49965/c

AA49965 standard; DNA; 28 BP.

XX AA49965;

DT 10-DEC-2002 (first entry)

DE B1153 expression in allergic disease related probe #1.

XX Human; allergy; B1153; differential expression; antiallergic; asthma;  
 KM antisthmatic; antiinflammatory; atopic skin inflammation; probe; ss.

XX Unidentified.

OS Unidentified.

XX Key Location/Qualifiers

FT modified\_base 1

FT modified\_base 1

FT modified\_base 1

FT modified\_base 1

FT modified\_base 1

FT modified\_base 1

FT modified\_base 1

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FT modified\_base 1

FT modified\_base 1

FT modified\_base 1

FT modified\_base 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 2356.15 seconds  
(without alignments)  
7897.122 Million cell updates/sec

Title: US-09-887-941B-5  
Perfect score: 384  
Sequence: 1 caggccgcgcgcgagactccac.....atgagtgctgggaccgcgcgt 384

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

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2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_ov:\*  
5: gb\_ov:\*  
6: gb\_pal:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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VERSION	BD171194.1				
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REFERENCE	other sequences; artificial sequences.				
AUTHORS	1 (bases 1 to 28)				
TITLE	Matsumoto,Y., Imai,Y., Oshida,T., Sugita,Y., Nagaau,T. and Tsujimoto,G.				
JOURNAL	Method of examining allergic disease				
	Patent: MO 0250269-A 19 27-JUN-2002;				

COMMENT

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PD	27-JUN-2002
PF	21-DEC-2001 WO 2001JP011286
PR	21-DEC-2000 JP 00P 389476
PI	YOSHIKO MATSUMOTO, YUKIHO IMAI, TADAHIRO OSHIDA, YUJI SUGITA, PI TAKESHI NAGASU,
PI	GOZO TSUJIMOTO
PC	C12N15/11, C07K16/18, A61K67/027, A61K31/711, A61K45/00, A61K48/00,
PC	A61P37/08,
PC	C12Q1/68, G01N33/50
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Key	location/Qualifiers
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ORIGIN

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DEFINITION	Identification of molecular interaction sites in RNA for novel drug discovery.

ACCESSION	BD274271
VERSION	BD274271.1
KEYWORDS	JP 2002526030-A/238.
SOURCE	synthetic construct
ORGANISM	synthetic construct
REFERENCE	other sequences; artificial sequences.
AUTHORS	1 (bases 1 to 42)
TITLE	Ecker,D.J., Sampath,R., Griffey,R. and Mcneil,J. Identification of molecular interaction sites in RNA for novel drugs
JOURNAL	Patent: JP 2002526030-A 238 20-AUG-2002;
COMMENT	ISIS PHARMACEUTICALS INC OS Artificial Sequence PN JP 2002526030-A/238

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BD274275  
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other sequences; artificial sequences.  
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Identification of molecular interaction sites in RNA for novel drug  
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PR	12-MAY-1998 US	60/068092,13-MAY-1998 US	09/076440	PI	
DAVID J ECKER,RANCA SAMPATH RICHARD GRIFFEY JOHN MCNEIL PC					
C12QI/68,A6IK31/7105,A61K48/00,C12N15/09,C12M15/00 CC					Description
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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US-10-751-736-7378

Sequence 7378, Application US/10751736  
Publication No. US20040265230A1

## GENERAL INFORMATION:

APPLICANT: Wyeth  
APPLICANT: Martinez, Robert  
APPLICANT: Brown, Eugene  
APPLICANT: Liu, Wei  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON  
FILE REFERENCE: AM100927 (031896-002000)  
CURRENT APPLICATION NUMBER: US/10/751,736  
CURRENT FILING DATE: 2003-01-06  
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000  
PRIOR FILING DATE: 2003-01-06  
NUMBER OF SEQ ID NOS: 54873  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 7378  
LENGTH: 21  
TYPE: DNA  
ORGANISM: homo sapiens  
US-10-751-736-7378

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US-10-751-736-7379

Sequence 7379, Application US/10751736  
Publication No. US20040265230A1

## GENERAL INFORMATION:

APPLICANT: Wyeth  
APPLICANT: Martinez, Robert  
APPLICANT: Brown, Eugene  
APPLICANT: Liu, Wei  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON  
FILE REFERENCE: AM100927 (031896-002000)  
CURRENT APPLICATION NUMBER: US/10/751,736  
CURRENT FILING DATE: 2003-01-06  
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000

PRIOR FILING DATE: 2003-01-06  
NUMBER OF SEQ ID NOS: 54873  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 7379  
LENGTH: 21  
TYPE: RNA  
ORGANISM: RNA1  
US-10-751-736-7379

Query Match 11.5%; Score 17; DB 20; Length 21;  
Best Local Similarity 94.1%; Pred. No. 56;  
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 33 GCAGCAGCAAGCCAAAT 49  
DB 3 GCAGCAGCAAGCCAAU 19

RESULT 3  
US-10-719-900-54731/C

Sequence 54731, Application US/10719900  
Publication No. US20050026164A1

## GENERAL INFORMATION:

APPLICANT: Xue Mei Zhou  
TITLE OF INVENTION: Methods of Genetic Analysis of Mouse  
FILE REFERENCE: 3528.1  
CURRENT APPLICATION NUMBER: US/10/719,900  
CURRENT FILING DATE: 2003-11-20  
PRIOR APPLICATION NUMBER: 60/427,808  
PRIOR FILING DATE: 2002 11 20  
NUMBER OF SEQ ID NOS: 982914  
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
SEQ ID NO 54731  
LENGTH: 25  
TYPE: DNA  
ORGANISM: Mus musculus  
US-10-719-900-54731

Query Match 11.5%; Score 17; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 CCTGTGCAGCAGCAAG 44  
DB 21 CCTGTGCAGCAGCAAG 5

RESULT 4  
US-10-751-736-6811

Sequence 6811, Application US/10751736  
Publication No. US20040265230A1

## GENERAL INFORMATION:

APPLICANT: Wyeth  
APPLICANT: Martinez, Robert  
APPLICANT: Brown, Eugene  
APPLICANT: Liu, Wei  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON  
FILE REFERENCE: AM100927 (031896-002000)  
CURRENT APPLICATION NUMBER: US/10/751,736  
CURRENT FILING DATE: 2003-01-06  
PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000  
NUMBER OF SEQ ID NOS: 54873  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 6811  
LENGTH: 21  
TYPE: DNA  
ORGANISM: homo sapiens  
US-10-751-736-6811

Query Match 10.8%; Score 16; DB 20; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2e+02;



## ALIGNMENTS

## RESULT 1

US-09-360-416-119  
; Sequence 119, Application US/09360416  
; Patent No. 6458536  
; GENERAL INFORMATION:  
; APPLICANT: Richard A. Gatti  
; TITLE OF INVENTION: METHODS FOR DETECTION OF ATAXIA  
; FILE REFERENCE: 510015-222  
; CURRENT APPLICATION NUMBER: US/09/360,416  
; CURRENT FILING DATE: 1999-07-23  
; NUMBER OF SEQ ID NOS: 143  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 119  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Human  
US-09-360-416-119

Query Match 10.1%; Score 15; DB 3; Length 20;  
Best Local Similarity 100.0%; Pred. No. 1.8e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 51 TATTTCATTCTTA 65  
|||||  
Db 5 TATTTCATTCTTA 19

## RESULT 2

US-08-160-670A-41  
; Sequence 41, Application US/08160670A  
; Patent No. 5449758  
; GENERAL INFORMATION:  
; APPLICANT: Hartley, James L.  
; TITLE OF INVENTION: Protein Size Marker Ladder  
; NUMBER OF SEQUENCES: 49  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/160,670A  
; FILING DATE: 12/2/93  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 0942.2580000  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2540  
; TELEFAX: (202) 371-2540  
; INFORMATION FOR SEQ ID NO: 41:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: both

US-08-160-670A-41

Query Match

10.1%; Score 15; DB 1; Length 30;

Best Local Similarity 100.0%; Pred. No. 1.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 66 TTTGAGTTGCCACC 80  
|||||  
Db 4 TTTGAGTTGCCACC 18

## RESULT 3

US-09-443-501A-8  
; Sequence 8, Application US/09443501A  
; Patent No. 6303342  
; GENERAL INFORMATION:  
; APPLICANT: Kusan Biosciences, Inc.  
; APPLICANT: Julien, Bryan  
; APPLICANT: Katz, Leonard  
; APPLICANT: Khosla, Chaitan  
; APPLICANT: Tang, Li  
; APPLICANT: Ziermann, Rainer  
; TITLE OF INVENTION: Recombinant Methods and Materials for Producing  
; FILE REFERENCE: 30062-20031.00  
; CURRENT APPLICATION NUMBER: US/09/443,501A  
; CURRENT FILING DATE: 1999-11-19  
; PRIOR APPLICATION NUMBER: US 60/130,560  
; PRIOR FILING DATE: 1999-04-22  
; PRIOR APPLICATION NUMBER: US 60/122,620  
; PRIOR FILING DATE: 1999-03-03  
; PRIOR APPLICATION NUMBER: US 60/119,386  
; PRIOR FILING DATE: 1999-02-10  
; PRIOR APPLICATION NUMBER: US 60/109,401  
; PRIOR FILING DATE: 1998-11-20  
; NUMBER OF SEQ ID NOS: 22  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic construct  
US-09-443-501A-8

Query Match 9.5%; Score 14; DB 3; Length 50;  
Best Local Similarity 100.0%; Pred. No. 7.1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 121 GACCGACCGAGAG 134  
|||||  
Db 24 GACCGACCGAGAG 37

## RESULT 4

US-09-357-072-78/C  
; Sequence 78, Application US/09357072  
; Patent No. 6015712  
; GENERAL INFORMATION:  
; APPLICANT: Brett P. Monia  
; APPLICANT: Brenda F. Baker  
; APPLICANT: Hong Zhang  
; APPLICANT: Lex M. Cowsett  
; TITLE OF INVENTION: ANTISENSE MODULATION OF PADD EXPRESSION  
; FILE REFERENCE: RTS-0027  
; CURRENT APPLICATION NUMBER: US/09/357,072  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 87  
; SEQ ID NO 78  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Antisense Oligonucleotide  
US-09-357-072-78



98 11 7.4 38 8 AZ382826 AZ382826 1M0140F13  
 99 11 7.4 38 8 AZ592469 AZ592469 1M0403K19  
 100 11 7.4 38 8 BZ380345 BZ380345 SALK\_1149

## ALIGNMENTS

RESULT 1  
 LOCUS A1444400 40 bp mRNA linear EST 07-JUN-2001  
 DEFINITION FB38a05.x1 Zebrafish Washu MP1MG EST Danio rerio cDNA clone  
 IMAGE:3714128.3 similar to SW:RS8\_HUMAN P09058 40S RIBOSOMAL  
 PROTEIN S8. /, mRNA sequence.  
 ACCESSION A1444400  
 VERSION A1444400.1 GI:4281397  
 KEYWORDS EST.  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Osteichthyes;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 40)  
 Clark, M., Johnson, S. L., Lehrach, H., Lee, R., Li, F., Marra, M.,  
 Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
 Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,  
 Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schuck, R.,  
 Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, W., McCann, R.,  
 Waterston, R., and Wilson, R.  
 Washu Zebrafish EST Project 1998  
 Unpublished (1998)  
 CONTACT: Stephen L. Johnson  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: zbrfish@wustl.wustl.edu  
 CDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:  
 Matthew Clark. DNA Sequencing by: Washington University Genome  
 Sequencing Center Clone distribution: Genome Systems, St. Louis,  
 Missouri (web address: www.genomesystems.com) (email contact:  
 info@genomesystems.com) and Research Genetics, Huntsville, Alabama  
 (web address: www.resgen.com) (email contact: info@resgen.com) and  
 Reesourcenzenzentrumpriatdatenbank, Berlin, Germany (web address:  
 www.rzpd.de)

Trace considered overall poor quality  
 Possible reversed clone; similarity on wrong strand  
 Seq primer: T7 ET from Amersham  
 High quality sequence stop: 1  
 POLYA=NO.

## FEATURES

location/Qualifiers  
 1..40  
 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /clone="IMAGE:3714128"  
 /sex="mixed"  
 /tissue-type="26 somite embryos, adult livers, shield  
 stage embryos"  
 /lab\_host="XLI-blue MRF"  
 /clone\_lib="Zebrafish Washu MP1MG EST"  
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st  
 strand cDNA was primed with a Not I - oligo(dT)15 primer  
 (5'-GACACTAGTCTAGATCGGAGCGCCGCCCTTTTCTTTTCTTTT3');  
 double-stranded cDNA was ligated to Sal I adaptor (BRL),  
 digested with Not I and cloned into the Not I and Sal I  
 sites of the pSPORT1 vector (BRL). Library was constructed  
 by Matthew Clark (Lehrach lab), ICRF, London and Max Planck  
 Institut fuer Molekulare Genetik, Berlin). cDNAs for EST  
 analysis were selected following oligonucleotide  
 hybridization fingerprinting of arrayed clones from  
 zebrafish late somitogenesis (26 som), adult liver or  
 embryonic shield stage (5.6 h) libraries. Fingerprint

## ORIGIN

Query Match 9.5%; Score 14; DB 1; Length 40;  
 Best Local Similarity 100.0%; Pred. No. 2.2e+04;  
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 74 TGCCACCAAAACAA 87  
 2 TGCCACCAAAACAA 15

data were used to computationally cluster cDNAs, and a  
 single cDNA from each cluster was chosen for sequencing.  
 In some cases multiple members of the same cluster were  
 sequenced to assess clustering parameters or single clones  
 were sequenced additional times to assess quality  
 control."

RESULT 2  
 LOCUS A2591573 44 bp DNA linear GSS 13-DEC-2000  
 DEFINITION 1M0401E18R Mouse 10kb plasmid UGCLIM library Mus musculus genomic  
 clone UGCLIM0401E15 R, genomic survey sequence.  
 ACCESSION A2591573  
 VERSION A2591573  
 KEYWORDS A2591573.1 GI:11713763  
 SOURCE GSS.  
 ORGANISM Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 44)  
 Dunn, D., Aoyagi, A., Barber, M., Beacom, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Rilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A., and Wright, D., Weiss, R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 Unpublished (2000)  
 CONTACT: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: dunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0401 row: B column: 15  
 Seq primer: CACACAGAAACAGCTATGACG  
 Class: Plasmid ends  
 High quality sequence stop: 44.

location/Qualifiers  
 1..44  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCLIM0401E15"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCLIM library"  
 /note="Vector: pMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passages through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

## FEATURES

location/Qualifiers  
 1..44  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UGCLIM0401E15"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UGCLIM library"  
 /note="Vector: pMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passages through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (gi|4732114|gb|AF129072.1), a copy-number

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 155.633 Seconds  
(without alignments)  
5629.394 Million cell updates/sec

Title: US-09-887-941B-4

Perfect score: 148  
Sequence: 1 ttgcgcgcagtcacgaac.....gagaagaagagctcccg 148

Scoring table: OLIGO\_NTIC  
Gapop 60.0, Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

1: N\_Geneseq\_16Dec04:\*  
2: geneseqn1980s:\*  
3: geneseqn1990s:\*  
4: geneseqn2000s:\*  
5: geneseqn2001as:\*  
6: geneseqn2001bs:\*  
7: geneseqn2002as:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	15	10.1	19	2	AAZ10229
C 2	15	10.1	20	4	AAF60217
C 3	15	10.1	30	2	AAT04991
C 4	14	9.5	20	10	ABZ94057
C 5	14	9.5	20	11	ABD30287
C 6	14	9.5	21	3	AAC64373
C 7	14	9.5	23	6	AAZ52722
C 8	14	9.5	25	6	AAZ27200
C 9	14	9.5	25	9	ACI16614
C 10	14	9.5	25	9	ACI14845
C 11	14	9.5	28	13	ADR32546
C 12	14	9.5	32	13	ADR33205
C 13	14	9.5	43	6	ABZ26875
C 14	14	9.5	50	3	AAA29355
C 15	13	8.8	13	5	ABC33708
C 16	13	8.8	13	5	ABC33709
C 17	13	8.8	17	3	AAF07081
C 18	13	8.8	17	8	ACA06862
C 19	13	8.8	17	8	ACA07862
C 20	13	8.8	17	8	ACA06821

C 21	13	8.8	17	8	ACC63011	ACC63011 Murine ol
C 22	13	8.8	19	12	ADF91918	ADF91918 Human cyf
C 23	13	8.8	19	12	ADF92115	ADF92115 Human cyf
C 24	13	8.8	19	12	ADG62153	ADG62153 Anti-FAD
C 25	13	8.8	19	13	ADR76043	ADR76043 Human apo
C 26	13	8.8	19	13	ADR78661	ADR78661 Human apo
C 27	13	8.8	20	2	AAT99894	AAT99894 Primer OM
C 28	13	8.8	20	2	AAT99895	AAT99895 Primer OM
C 29	13	8.8	20	2	AAT99896	AAT99896 Primer OM
C 30	13	8.8	20	2	AAT98089	AAT98089 Chlamydia
C 31	13	8.8	20	2	AAT98091	AAT98091 Chlamydia
C 32	13	8.8	20	3	AAZ44822	AAZ44822 Human FAD
C 33	13	8.8	20	3	AAA17901	AAA17901 Chlamydia
C 34	13	8.8	20	3	AAA65807	AAA65807 Chlamydia
C 35	13	8.8	20	3	AAA65808	AAA65808 Chlamydia
C 36	13	8.8	20	4	AAH02989	AAH02989 C trachom
C 37	13	8.8	20	4	AAH02990	AAH02990 C trachom
C 38	13	8.8	20	4	AAH02991	AAH02991 C trachom
C 39	13	8.8	20	4	AAH02992	AAH02992 Human GU
C 40	13	8.8	20	8	ABT15797	ABT15797 Human GU
C 41	13	8.8	20	9	ACF05746	ACF05746 Bcl2 sens
C 42	13	8.8	20	9	ADA27414	ADA27414 Micoorgan
C 43	13	8.8	20	9	ADA27415	ADA27415 Micoorgan
C 44	13	8.8	20	9	ADA27413	ADA27413 Micoorgan
C 45	13	8.8	20	10	ABZ94058	ABZ94058 Human ol
C 46	13	8.8	20	11	ABD30288	ABD30288 H05914-de
C 47	13	8.8	20	12	ADF91920	ADF91920 Human cyf
C 48	13	8.8	20	12	ADF91919	ADF91919 Human cyf
C 49	13	8.8	20	12	ADF92116	ADF92116 Human cyf
C 50	13	8.8	20	12	ADG86687	ADG86687 Human APP
C 51	13	8.8	21	12	AD016005	AD016005 4 synthes
C 52	13	8.8	22	12	ADK41285	ADK41285 Human chr
C 53	13	8.8	22	12	ADK41395	ADK41395 Human chr
C 54	13	8.8	22	12	ADK41395	ADK41395 Human chr
C 55	13	8.8	23	6	ABT08556	ABT08556 Human nov
C 56	13	8.8	23	8	AA154151	AA154151 NOV rela
C 57	13	8.8	23	12	AD009921	AD009921 Human NOV
C 58	13	8.8	23	12	AD041932	AD041932 Novel hum
C 59	13	8.8	24	6	ABK69681	ABK69681 Human WTI
C 60	13	8.8	24	6	ABZ30370	ABZ30370 Candida a
C 61	13	8.8	24	6	ABK61809	ABK61809 Analyt e
C 62	13	8.8	24	6	AB187774	AB187774 Capture o
C 63	13	8.8	24	6	AB187775	AB187775 Capture o
C 64	13	8.8	24	10	ADB67557	ADB67557 Human WTI
C 65	13	8.8	24	10	ADB80790	ADB80790 Wilms tu
C 66	13	8.8	24	12	ADU83710	ADU83710 PCR prime
C 67	13	8.8	24	12	ADU57598	ADU57598 Human tru
C 68	13	8.8	25	12	AD009153	AD009153 Truncated
C 69	13	8.8	25	9	ACI65526	ACI65526 Human mic
C 70	13	8.8	25	9	ACI11414	ACI11414 Human mic
C 71	13	8.8	25	9	ACI112050	ACI112050 Human mic
C 72	13	8.8	25	9	ACK08719	ACK08719 Human mic
C 73	13	8.8	25	9	ACI24980	ACI24980 Human mic
C 74	13	8.8	25	9	ACI15507	ACI15507 Human mic
C 75	13	8.8	25	9	ACI10776	ACI10776 Human mic
C 76	13	8.8	25	9	ACI10140	ACI10140 Human mic
C 77	13	8.8	25	9	ACI194368	ACI194368 Human mic
C 78	13	8.8	25	9	ACH51016	ACH51016 DNA targe
C 79	13	8.8	25	9	ACH52593	ACH52593 DNA targe
C 80	13	8.8	25	9	ACH51015	ACH51015 DNA targe
C 81	13	8.8	25	12	ADN96735	ADN96735 Human NOV
C 82	13	8.8	25	12	ADN16726	ADN16726 Renal cel
C 83	13	8.8	25	12	ADP16724	ADP16724 Renal cel
C 84	13	8.8	25	12	ADP16725	ADP16725 Renal cel
C 85	13	8.8	25	12	ADP16725	ADP16725 Renal cel
C 86	13	8.8	26	6	ABK66694	ABK66694 Human gen
C 87	13	8.8	27	10	ADK17672	ADK17672 HeLa cell
C 88	13	8.8	30	6	ABK67581	ABK67581 Novel Hei
C 89	13	8.8	32	6	ABK16403	ABK16403 Human adi
C 90	13	8.8	32	12	AAA15731	AAA15731 PCR prime
C 91	13	8.8	33	3	ABK48783	ABK48783 PCR prime
C 92	13	8.8	33	6	ABK50828	ABK50828 Cyclin de
C 93	13	8.8	35	3	ABK50828	ABK50828 Cyclin de

	94	13	8.8	35	4	AAf24618
C	95	13	8.8	36	2	AAV46359
C	96	13	8.8	36	12	ADf92158
C	97	13	8.8	37	12	ADf92158
C	98	13	8.8	39	4	AAf24615
C	99	13	8.8	41	6	ABZ46601
C	100	13	8.8	41	6	ABZ44247

## ALIGNMENTS

## RESULT 1

AAZ10229/c  
ID AAZ10229 standard; DNA, 19 BP.

AA210229;

01-NOV-1999 (first entry)

Oligonucleotide probe P6 used to detect a Met receptor.

Hepatocyte growth factor; HGF; axonal growth; sympathetic neuron;  
axonal regeneration; axonal degeneration; post-natal neuron; neuropathy;  
motor neuropathy; diabetic neuropathy; distal sensory; sensorimotor;  
autonomic; visceral autonomic polynuropathy; mononeuropathy;  
mononeuropathy multiplex; foot ulceration; cardiac arrhythmia;  
sexual impotence; chronic pain; abnormal vascular response; infection;  
ischemia; toxin exposure; radiation; Met receptor; probe; ss.

Synthetic.

Mus sp.

WO936103-A1.

22-JUL-1999.

15-JAN-1999; 99MO-US000965.

16-JAN-1998; 98US-00071694.

(UYMC-) UNIV MCGILL.

Miller FD, Yang X;

WPI; 1999-527196/44.

Novel methods for preventing axonal degeneration and promoting axonal growth using hepatocyte growth factor.

Example 1; Page 21; 65pp; English.

The present sequence represents a probe used to detect a Met receptor. The Met receptor is the cognate receptor for hepatocyte growth factor (HGF), which is used to promote axonal growth. Localized exogenous HGF promotes the growth (but not the survival) of sympathetic neurons. HGF specification describes a method for promoting axonal growth or axonal regeneration, or for inhibiting axonal degeneration, of a post-natal neuron. The method comprises administering an expression vector, comprising HGF gene operably linked to a promoter, to the neuron. HGF may be used for treating or inhibiting neuropathy in a patient. The neuropathy may be symptomatic or asymptomatic, caused by axonal degeneration, and is an autonomic, sensory, a sensorimotor or a motor neuropathy and a diabetic neuropathy (especially distal sensory, sensorimotor, autonomic and visceral autonomic polynuropathy, and mononeuropathy, or mononeuropathy multiplex). HGF may also be used in the treatment of foot ulceration, cardiac arrhythmia, sexual impotence, chronic pain or abnormal vascular responses. HGF may be used to promote axonal growth and regeneration, for the prevention or treatment of neuropathies involving axonal degeneration, e.g. infection, ischemia, toxin exposure, radiation

Sequence 19 BP; 1 A; 5 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 10.1%; Score 15; DB 2; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1e+03;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

33 GCAGCAGCAAGCCA 47  
15 GCAGCAGCAAGCCA 1

## RESULT 2

AAF60217  
ID AAF60217 standard; DNA, 20 BP.

AAF60217;

27-APR-2001 (first entry)

Human ATM gene exon 53 reverse primer.

Human; ATM; ataxia telangiectasia; mutation detection;

single-stranded conformation polymorphism; SSCP; electrophoresis;

PCR primer; ss.

Homo sapiens.

WO200107660-A1.

01-FEB-2001.

21-JUL-2000; 2000WO-US020011.

23-JUL-1999; 99US-00360416.

(REGC) UNIV CALIFORNIA.

Gatti RA;

WPI; 2001-168574/17.

Claim 7; Page 54; 118pp; English.

The present sequence is one of a number of primers used in a method for detecting a mutation or a polymorphism in the human ATM gene, which is associated with the disease ataxia telangiectasia, or a polyexonic eukaryotic gene of at least 4 kb. The method uses an improved version of single-stranded conformation polymorphism (SSCP) electrophoresis that allows electrophoresis of two or three amplified segments in a single lane. The method is useful for screening large, complex polyexonic eukaryotic genes such as the ATM gene for mutations and polymorphisms. The new mutations and polymorphisms in the ATM gene are useful for performing more accurate screening of human DNA samples for mutations, for distinguishing mutations from polymorphisms, and for improving the efficiency of automated screening methods. The mega-SSCP method provides a screening method of genes for multiple polymorphisms and mutations at once. The method is particularly suitable for large, polyexonic, eukaryotic genes, having mutations and polymorphisms at many points and not merely at one or a few hot spots. Note: the SEQ ID assigned to this sequence in the disclosure and claims of the specification is one number lower than the number given in the sequence listing

Sequence 20 BP; 3 A; 3 C; 2 G; 12 T; 0 U; 0 Other;

Query Match 10.1%; Score 15; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.1e+03;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

51 TATTCATTTCTTA 65

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OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 908.099 Seconds  
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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
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Post-processing: Listing first 100 summaries

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14: gb\_vl: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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6	14	9.5	43	6	AX483454
7	14	9.5	50	6	AR172670
8	14	9.5	50	6	BD251448
9	13	8.8	17	6	BD259279
10	13	8.8	17	6	AX722571
11	13	8.8	20	6	AR101728
12	13	8.8	20	6	AR101729
13	13	8.8	20	6	AR101730
14	13	8.8	20	6	AR266147
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16	13	8.8	20	6	AX800101
17	13	8.8	20	6	AX926413
18	13	8.8	22	6	CQ760601
19	13	8.8	22	6	CQ760711

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C 24	13	8.8	25	6	AR239337	AR239337 Sequence
C 25	13	8.8	25	6	AX279139	AX279139 Sequence
C 26	13	8.8	26	6	AR090662	AR090662 Sequence
C 27	13	8.8	26	6	AR197697	AR197697 Sequence
C 28	13	8.8	26	6	AR259851	AR259851 Sequence
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C 44	12	8.1	15	6	AR056324	AR056324 Sequence
C 45	12	8.1	15	6	AR056327	AR056327 Sequence
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C 77	12	8.1	17	6	AX733934	AX733934 Sequence
C 78	12	8.1	17	6	AX734775	AX734775 Sequence
C 79	12	8.1	18	6	A61371	A61371 Sequence
C 80	12	8.1	18	6	BD196440	BD196440 Prostatic
C 81	12	8.1	18	6	BD196724	BD196724 Prostatic
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C 89	12	8.1	19	6	AX129455	AX129455 Sequence
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 96 12 8.1 20 6 AR035747 Sequence AR035747 Sequence  
 97 12 8.1 20 6 AR044967 Sequence AR044967 Sequence  
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## ALIGNMENTS

RESULT 1 20 bp DNA linear MAM 06-FEB-1999  
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 DEFINITION Bovine DNA for microsatellite marker, 3' terminus.  
 ACCESSION D83323  
 VERSION D83323.1 GI:1199740  
 KEYWORDS PCR primer.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovinae; Bos.  
 1 (sites)  
 Hitano,T., Nakane,S., Mizoshita,K., Yamakuchi,H.,  
 Inoue-Murayama,M., Watanabe,T., Barendse,W. and Sugimoto,Y.  
 Characterization of 42 highly polymorphic bovine microsatellite  
 markers  
 JOURNAL Anim. Genet. 27 (5), 365-368 (1996)  
 MEDLINE 97083737  
 PUBMED 8930081  
 2 (bases 1 to 20)  
 Hitano,T., Nakane,S., Mizoshita,K., Inoue-Murayama,M., Watanabe,T.,  
 Barendse,W. and Sugimoto,Y.  
 Characterization of 42 bovine microsatellite markers  
 TITLE Unpublished  
 JOURNAL 3 (bases 1 to 20)  
 SUGIMOTO,Y.  
 Direct Submission  
 Submitted (29-JAN-1996) Yoshikazu Sugimoto, Japan Live Stock  
 Technology Association, Shikawa Institute of Animal Genetics;  
 Nishio Oshikura, Nishihirakawa, Fukushima 961, Japan  
 (E-mail:LDI03222@niftyserve.or.jp, Tel:0246-25-5641,  
 Fax:0248-25-5725)  
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 1 GCCTGAGGCGAGAA 15  
 RESULT 2 20 bp DNA linear PAT 20-DEC-2002  
 LOCUS AR233757  
 DEFINITION Sequence 119 from patent US 6458536.  
 ACCESSION AR233757  
 VERSION AR233757.1 GI:27276381  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.

Unclassified.  
 1 (bases 1 to 20)  
 Gatti,R.A.  
 Modified SSCP method using sequential electrophoresis of multiple  
 nucleic acid segments  
 JOURNAL Patent: US 6458536-A 119 01-OCT-2002;  
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 RESULT 3 30 bp DNA linear PAT 26-SEP-1995  
 LOCUS I14415  
 DEFINITION Sequence 41 from patent US 5449758.  
 ACCESSION I14415  
 VERSION I14415.1 GI:996901  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 1 (bases 1 to 30)  
 Hartley,J.L.  
 Protein size marker ladder  
 Patent: US 5449758-A 41 12-SEP-1995;  
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 LOCUS BD275574  
 DEFINITION Novel Human Voltage-Gated Potassium Channel.  
 ACCESSION BD275574  
 VERSION BD275574.1 GI:33085342  
 KEYWORDS JP 2002543768-A/4.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 21)  
 Metzker,M.L., Li,W., Petrukhn,K. and Caskey,T.C.  
 Novel Human Voltage-Gated Potassium Channel  
 Patent: JP 2002543768-A 4 24-DEC-2002;  
 COMMENT  
 OS Homo Sapiens  
 PN JP 2002543768-A/4  
 PD 24-DEC-2002  
 PF 10-APR-2000 JP 2000611548  
 PR 14-APR-1999 US 60/129274  
 PI Michael I metzker,wen li,konstantin petrukhn,thomas c caskey  
 CC

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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a  
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#### SUMMARIES

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C 5	15	8.5	20	US-10-829-674-386	Sequence 386, App
C 6	15	8.5	20	US-10-830-477-386	Sequence 386, App
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C 12	15	8.5	25	US-10-719-956-603885	Sequence 603885,
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C 16	14	7.9	21	US-10-751-736-15076	Sequence 15076, A
C 17	14	7.9	21	US-10-751-736-15077	Sequence 15077, A
C 18	14	7.9	21	US-09-888-0564-27	Sequence 27, Appl
C 19	14	7.9	23	US-10-362-091-19	Sequence 19, Appl
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84 14 7.9 25 24 US-11-036-317-825774 Sequence 825774.
85 14 7.9 25 24 US-11-036-317-906120 Sequence 906120.
86 14 7.9 26 17 US-10-381-779-75 Sequence 35, App1
87 14 7.9 33 15 US-10-079-709-35 Sequence 3070, Ap
88 13 7.3 17 10 US-09-818-875-3070 Sequence 3071, Ap
89 13 7.3 17 10 US-09-818-875-3071 Sequence 3070, Ap
90 13 7.3 17 17 US-10-209-787-3070 Sequence 3071, Ap
91 13 7.3 17 17 US-10-209-787-3071 Sequence 3070, Ap
92 13 7.3 17 17 US-10-261-185-3070 Sequence 3071, Ap
93 13 7.3 17 17 US-10-261-185-3071 Sequence 3070, Ap
94 13 7.3 17 19 US-10-681-074-3070 Sequence 3071, Ap
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96 13 7.3 18 17 US-10-349-607-96 Sequence 96, App1
97 13 7.3 19 17 US-10-444-925-88 Sequence 89, App1
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100 13 7.3 19 17 US-10-444-925-226
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## ALIGNMENTS

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; Sequence 435950, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 435950
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-435950
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 25 CTCCTGTTCCGAGCTA 9
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US-11-036-317-939697
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; Sequence 939697, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 939697
; LENGTH: 25
; TYPE: DNA
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; ORGANISM: Mus musculus
US-11-036-317-939697
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 2 CCTCCGAGGCGCAGCC 18
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US-11-036-317-980948
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; Sequence 980948, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; PRIOR FILING DATE: 2004-01-13
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 980948
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-11-036-317-980948
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 4 CCTCCGAGGCGCAGCC 20
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RESULT 4
US-10-085-188-4/C
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; Sequence 4, Application US/10085188
; Publication No. US20030032778A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Taft, David W.
; TITLE OF INVENTION: A New Member of the Human
; FILE REFERENCE: 98-69
; CURRENT APPLICATION NUMBER: US/10/085,188
; CURRENT FILING DATE: 2002-02-26
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR primer
US-10-085-188-4
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Query Match
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 18 TTCCACGACGACG 4
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using ew model

Run on: October 7, 2005, 23:25:05 ; Search time 54.315 Seconds  
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Title: US-09-887-941B-3

Perfect score: 177

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Gapop 60.0 , Gapext 60.0

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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 84	12	6.8	25 2 US-08-468-042C-4	Sequence 2, Appl
C 85	12	6.8	25 3 US-08-748-130-29	Sequence 29, Appl
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## ALIGNMENTS

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RESULT 1
US-09-693-555A-13
Sequence 13, Application US/09693555A
Patent No. 6733967
GENERAL INFORMATION:
APPLICANT: KORNMANN, KENNETH
APPLICANT: DUFF, GORDON
APPLICANT: OFFENBACHER, STEVEN
TITLE OF INVENTION: FETAL TESTING FOR PREDICTION OF LOW BIRTH WEIGHT
FILE REFERENCE: MSA-009.01
CURRENT APPLICATION NUMBER: US/09/693,555A
CURRENT FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: PCT/US99/08794
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: 60/082,487
PRIOR FILING DATE: 1998-04-21
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-693-555A-13

Query Match          7.9%; Score 14; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      118 GAAGCCCTCCGAG 131
DB      1 GAAGCCCTCCGAG 14

RESULT 2
US-07-923-724-12/c
Sequence 12, Application US/07923724
Patent No. 5780292
GENERAL INFORMATION:
APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m, Richard B.
TITLE OF INVENTION: Production of Phylase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Cimbal, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050.0240004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: both
US-07-923-724-12

Query Match          7.9%; Score 14; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      24 CTCGACCGACGACCG 11
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RESULT 3
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Sequence 12, Application US/08609426A
Patent No. 5830733
GENERAL INFORMATION:
APPLICANT: Nevalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fagerstr m, Richard B.
APPLICANT: Houston, Christine S.
TITLE OF INVENTION: Production of Phylase Degrading Enzymes
TITLE OF INVENTION: in Trichoderma
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,426A
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-09-887-941B-3

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Word size : 0

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0  
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Post-processing: Listing first 100 summaries

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7: gb\_est6:  
8: gb\_gse1:  
9: gb\_gse2:

Pred. No. is the number of results predicted by chance to have a  
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and is derived by analysis of the total score distribution.

# SUMMARIES

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6	13	7.3	32	4	BZ357532 SALK_1308
7	13	7.3	33	4	BI829654 603079396
8	13	7.3	33	4	CC796535 SALK_1323
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13	13	7.3	47	8	BH791798 SALK_0613
14	13	7.3	50	1	AUI05516 AUI05516
15	13	7.3	50	4	BI830809 603080922
16	13	7.3	50	1	BI830809 603080922
17	13	7.3	50	1	AZ473371 IM0289A18
18	13	7.3	50	1	CL883203 GC0442.TI
19	13	7.3	50	1	AZ588245 IM0396N20
20	13	7.3	50	1	AZ439064 IM0229D06
21	13	7.3	50	1	BH811125 SALK_0574
22	13	7.3	50	1	BH910667 SALK_0610
23	13	7.3	50	1	AL987462 Dario rer
24	13	7.3	50	1	R89782 YP91d03.r1
25	13	7.3	50	1	AU257486 AU257486
26	13	7.3	50	1	BI915316 603184602

25	12	6.8	36	9	CL213814
26	12	6.8	38	1	AU256105
27	12	6.8	38	4	BJ063802
28	12	6.8	40	1	AI810174
29	12	6.8	41	8	BZ291498
30	12	6.8	41	9	TAI75A080
31	12	6.8	43	8	BH862454
32	12	6.8	46	1	AA717367
33	12	6.8	47	8	AZ852673
34	12	6.8	48	8	BH904917
35	12	6.8	50	1	AUI05546
36	12	6.8	50	6	CD532122
37	12	6.8	50	8	AZ510728
38	12	6.8	50	9	BH221751
39	12	6.8	50	9	CR235318
40	12	6.8	50	9	BG925573
41	12	6.2	16	4	AI476315
42	12	6.2	19	1	AZ595016
43	12	6.2	19	8	AZ834038
44	12	6.2	20	8	AZ611386
45	12	6.2	20	9	AG201710
46	12	6.2	20	9	AG202306
47	12	6.2	21	8	AZ812972
48	12	6.2	21	8	AZ640656
49	12	6.2	22	8	CF318495
50	12	6.2	23	7	AZ828350
51	12	6.2	24	8	AZ463313
52	12	6.2	24	8	BH910038
53	12	6.2	24	9	PCH304073
54	12	6.2	25	8	AZ646723
55	12	6.2	25	8	AZ824843
56	12	6.2	25	9	CC794288
57	12	6.2	27	1	AU260098
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61	12	6.2	28	8	AZ460864
62	12	6.2	28	8	AZ623636
63	12	6.2	29	8	AZ803607
64	12	6.2	29	8	AZ828692
65	12	6.2	29	8	BH840479
66	12	6.2	30	4	BU051129
67	12	6.2	30	8	AZ498972
68	12	6.2	30	8	AZ821583
69	12	6.2	30	8	AZ870335
70	12	6.2	30	8	AZ959340
71	12	6.2	30	1	AI158929
72	12	6.2	31	1	AI199731
73	12	6.2	31	8	BI809695
74	12	6.2	31	8	BH903544
75	12	6.2	31	8	BH903544
76	12	6.2	32	8	BZ763711
77	12	6.2	32	8	AZ819863
78	12	6.2	33	9	BX894791
79	12	6.2	33	9	AI536661
80	12	6.2	34	1	AV847122
81	12	6.2	34	1	AJ587076
82	12	6.2	34	9	CL528702
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93	12	6.2	37	8	AZ458505
94	12	6.2	38	8	CG785132
95	12	6.2	38	9	CL234430
96	12	6.2	38	9	CL234430
97	12	6.2	38	9	CL234430

CL213814	M046F07 G
AU256105	AU256105
BJ063802	BJ063802
AI810174	wf80e11.x
BZ291498	SALK_1208
TAI75A080	T. Bruce
BH862454	SALK_0899
AA717367	m210h12.r
AZ852673	2M0155X19
BH904917	SALK_1053
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BH221751	1006103B0
CR235318	Forward s
BG925573	HNC5-1-D8
AI476315	ta15c09.x
AZ595016	IM0407C19
AZ834038	2M0116H01
AZ611386	IM0437N08
AG201710	Pan tceq1
AG202306	Pan tceq1
AZ323997	IM0045B18
AZ810722	2M0074012
AZ640656	IM0502X14
CF318495	HD--08-K0
AZ828350	2M0105116
AZ463313	IM0272L03
BH910038	SALK_0573
PCH304073	Plasmid
AZ646723	IM0512F19
AZ824843	2M0099N08
CC794288	SALK_0468
AU260098	AU260098
AZ495352	IM0331E14
AA884882	am21e08.s
AI697335	lq18a01.x
AZ460864	IM0261N22
AZ623636	IM0461N05
AZ803607	2M0064A10
AZ828692	2M0105N15
BH840479	KG01991-3
BU051129	BU051129
AZ498972	IM0336D06
AZ821583	2M0094123
AZ870335	2M0182H15
AZ959340	2M0281E11
AI158929	qb57c08.x
AI199731	q158c05.x
AI801729	l094f03.x
BH809695	SALK_0049
BH903544	SALK_1028
BZ763711	601774306
AZ819863	2M0091D14
BX894791	Arabidops
AI536661	l014f10.x
AV847122	AV847122
AJ587076	Arabidops
CL528702	ASV3F12.f
BH865701	SALK_0977
AJ667672	AJ667672
T65804	ycl1h12.b1
AZ849598	2M0151P06
CR395129	Arabidops
AA878791	o582e05.s
AI085631	oz43d12.x
AI109482	sb74e12.y
AV836242	AV836242
AZ458505	IM0262107
AZ471063	IM0285005
CG785132	0050119-0
CL234430	0250422-0

98 11 6.2 39 4 BU065029 BU065029  
99 11 6.2 39 9 AG202285 AG202285 Pen trogl  
100 11 6.2 39 9 AL943780 AL943780 Arabidops

## ALIGNMENTS

RESULT 1  
LOCUS AI955350 37 bp mRNA linear EST 19-AUG-1999  
DEFINITION wcl1d12.x1 NCI CGAP Utl Homo sapiens cDNA clone IMAGE:2507159 3'  
similar to SW:MLH1\_HUMAN P40692 MUTL PROTEIN HOMOLOG 1, mRNA  
sequence.

ACCESSION AI955350 GI:5747660  
VERSION AI955350.1  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 37)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/btrp/image/image.html

Trace considered overall poor quality  
Seq primer: -40UP from Gibco  
High quality sequence stop: 1.

FEATURES  
source Location/Qualifiers

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/db\_xref="taxon:9606"  
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/tissue\_type="well-differentiated endometrial  
adenocarcinoma, 7 pooled tumors"  
/lab\_host="DH10B"  
/clone\_lib="NCI CGAP Utl1"  
/note="Organ: uterus; Vector: pCMV-SPORT6; Site\_1: Salt;  
Site\_2: NotI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.75 kb. Life Technologies catalog #: 11538-014"

## ORIGIN

Query Match 7.3%; Score 14; DB 1; Length 37;  
Best Local Similarity 100.0%; Pred. No. 3.7e+04;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 84 CTCGATCTTTGAA 97  
|||||  
10 CTCGATCTTTGAA 23

RESULT 2  
LOCUS BI762555/c 32 bp mRNA linear EST 25-SEP-2001  
DEFINITION 603048685F1 NIH\_MGC\_116 Homo sapiens cDNA clone IMAGE:5188724 5',  
mRNA sequence.  
ACCESSION BI762555  
VERSION BI762555.1 GI:15754133  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 32)  
NIH-MGC http://mgs.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L14M11471 row: 3 column: 21  
High quality sequence stop: 32.

FEATURES  
source Location/Qualifiers

1..32  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5188724"  
/lab\_host="DH10B"  
/clone\_lib="NIH\_MGC\_116"  
/note="Organ: pooled colon, kidney, stomach; Vector:  
pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA  
source anonymous pool of 3 colons, age 26 yo male, 49 yo  
female, 71 yo male colon; 46 yo male kidney, and pool of 2  
stomachs, 62 yo male and 70 yo female. Library is  
oligo-dt primed and directionally cloned (EcoRV site is  
destroyed upon cloning). Average insert size 1.4 kb,  
insert size range 1-3 kb. Library is normalized and  
enriched for full-length clones and was constructed by C.  
Gruber (Invitrogen). Research Genetics tracking code  
023. Note: this is a NIH\_MGC library."

## ORIGIN

Query Match 7.3%; Score 13; DB 4; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.2e+05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 81 TGCCCTCATCTTT 93  
|||||  
14 TGCCCTCATCTTT 2

RESULT 3  
LOCUS BI832949/c 32 bp mRNA linear EST 04-OCT-2001  
DEFINITION 603090781F1 NIH\_MGC\_120 Homo sapiens cDNA clone IMAGE:5229556 5',  
mRNA sequence.

ACCESSION BI832949  
VERSION BI832949.1 GI:15944499  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 32)  
NIH-MGC http://mgs.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 186.129 seconds  
(without alignments)  
5629.394 Million cell updates/sec

Title: US-09-887-941B-3

Perfect score: 177  
Sequence: 1 gcttcctttctcgcgttc.....gggaactgcctcctcgcctcg 177

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

N\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001as:\*  
5: Geneseq2001bs:\*  
6: Geneseq2002as:\*  
7: Geneseq2002bs:\*  
8: Geneseq2003as:\*  
9: Geneseq2003bs:\*  
10: Geneseq2003cs:\*  
11: Geneseq2003ds:\*  
12: Geneseq2004as:\*  
13: Geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	9.0	32	8	AAD50042 Human F1d
2	15	8.5	18	8	ABX10978 Human Zep
3	14	7.9	17	8	ADA99413 Human MDZ
4	14	7.9	17	8	ADA99411 Human MDZ
5	14	7.9	17	8	ADA99412 Human MDZ
6	14	7.9	17	8	ADA99410 Human MDZ
7	14	7.9	20	10	ACF79692 Sense prt
8	14	7.9	23	3	AAZ37214 PCR prime
9	14	7.9	23	3	AAC63789 Human TNF
10	14	7.9	23	6	AAD27403 Human tum
11	14	7.9	24	2	AAQ58130 cbhl-Phyt
12	14	7.9	24	6	AAI32967 Pear beta
13	14	7.9	25	8	ADB00914 Human MDZ
14	14	7.9	25	8	ADB00921 Human MDZ
15	14	7.9	25	8	ADB00919 Human MDZ
16	14	7.9	25	8	ADB00913 Human MDZ
17	14	7.9	25	8	ADB00915 Human MDZ
18	14	7.9	25	8	ADB00918 Human MDZ
19	14	7.9	25	8	ADB00912 Human MDZ
20	14	7.9	25	8	ADB00912 Human MDZ

21	14	7.9	25	8	ADB00920	ADB00920 Human MDZ
22	14	7.9	25	8	ADB00917	ADB00917 Human MDZ
23	14	7.9	25	8	ADB00910	ADB00910 Human MDZ
24	14	7.9	25	8	ADB00916	ADB00916 Human MDZ
25	14	7.9	25	9	ACK10775	ACK10775 Human mic
26	14	7.9	26	3	AAZ51522	AAZ51522 Control e
27	14	7.9	26	6	AAI40163	AAI40163 Isoprenol
28	14	7.9	26	12	ADQ07948	ADQ07948 Antisense
29	14	7.9	29	13	ADR32545	ADR32545 Human nic
30	14	7.9	33	2	AAE61845	AAE61845 Phytase g
31	14	7.9	33	2	AAE61882	AAE61882 A. niger
32	14	7.9	35	3	AAC63569	AAC63569 MiniSeqe
33	14	7.9	50	4	AAI30967	AAI30967 Human SNP
34	13	7.3	15	2	AAZ52877	AAZ52877 Adenosine
35	13	7.3	15	3	AAA32321	AAA32321 A3 adenos
36	13	7.3	15	3	AAA03715	AAA03715 Human ade
37	13	7.3	15	3	AAE18442	AAE18442 Human ade
38	13	7.3	15	3	AAA99534	AAA99534 Adenosine
39	13	7.3	15	4	AAE46398	AAE46398 IGFBP2 o1
40	13	7.3	15	4	AAE46397	AAE46397 IGFBP2 o1
41	13	7.3	15	4	AAE46399	AAE46399 IGFBP2 o1
42	13	7.3	15	10	ABZ94136	ABZ94136 Human pho
43	13	7.3	15	11	ABD32528	ABD32528 Al/A3 ant
44	13	7.3	17	4	ABA80224	ABA80224 MLH1 muta
45	13	7.3	17	4	ABA80225	ABA80225 MLH1 muta
46	13	7.3	17	8	ADA99414	ADA99414 Human MDZ
47	13	7.3	17	8	ADA99409	ADA99409 Human MDZ
48	13	7.3	17	10	ADI50192	ADI50192 Human tum
49	13	7.3	18	2	AAQ90905	AAQ90905 hMLH1 gen
50	13	7.3	18	3	AAA38359	AAA38359 Human Ets
51	13	7.3	18	3	AAE72228	AAE72228 Single nu
52	13	7.3	18	4	AAH26538	AAH26538 Human pro
53	13	7.3	19	2	AAE76054	AAE76054 Human Nid
54	13	7.3	19	11	ADL70053	ADL70053 Human GIP
55	13	7.3	19	11	ADL69940	ADL69940 Human GIP
56	13	7.3	19	12	ADH01541	ADH01541 Protein t
57	13	7.3	19	12	ADH01477	ADH01477 Human pro
58	13	7.3	19	12	ADH01476	ADH01476 Human pro
59	13	7.3	19	12	ADH01614	ADH01614 Protein t
60	13	7.3	19	12	ADN75743	ADN75743 PRPB ass
61	13	7.3	19	12	ADN75742	ADN75742 PRPB ass
62	13	7.3	20	2	AAQ87113	AAQ87113 Aspergill
63	13	7.3	20	2	AAE65602	AAE65602 PCR prime
64	13	7.3	20	5	AAE22295	AAE22295 Human COL
65	13	7.3	20	6	ABL45285	ABL45285 Human chr
66	13	7.3	20	6	AAAD4828	AAAD4828 Human raf
67	13	7.3	20	6	AB197537	AB197537 Capture o
68	13	7.3	20	8	ADA00937	ADA00937 Human Ras
69	13	7.3	20	9	ABT44394	ABT44394 ChimERIC
70	13	7.3	20	10	ACD42144	ACD42144 Human raf
71	13	7.3	21	4	AAE45504	AAE45504 Primer fo
72	13	7.3	21	10	ACF79746	ACF79746 Human ant
73	13	7.3	21	12	ADH01478	ADH01478 Human pro
74	13	7.3	21	12	ADH01475	ADH01475 Human pro
75	13	7.3	21	12	ADH01479	ADH01479 Human pro
76	13	7.3	21	12	ADN75745	ADN75745 PRPB ass
77	13	7.3	21	12	ADN75744	ADN75744 PRPB ass
78	13	7.3	21	12	ADN75741	ADN75741 Human prp
79	13	7.3	23	3	AAZ87370	AAZ87370 Hepatitis
80	13	7.3	24	6	AB191644	AB191644 Capture o
81	13	7.3	24	6	AB191645	AB191645 Capture o
82	13	7.3	25	8	ADB00922	ADB00922 Human MDZ
83	13	7.3	25	8	ADB00909	ADB00909 Human MDZ
84	13	7.3	25	9	ACK17044	ACK17044 Human mic
85	13	7.3	25	9	ACK19756	ACK19756 Human mic
86	13	7.3	25	9	ACK25519	ACK25519 Human mic
87	13	7.3	25	9	ACK25519	ACK25519 Human mic
88	13	7.3	27	6	AAI40165	AAI40165 Isoprenol
89	13	7.3	29	8	ABO83220	ABO83220 Coffee Rb
90	13	7.3	29	12	ADP18514	ADP18514 Synthetic
91	13	7.3	31	4	AAI31001	AAI31001 Human sin
92	13	7.3	33	10	ACC49803	ACC49803 Human myo
93	13	7.3	35	10	ADC35659	ADC35659 Dehydroge



94	13	7.3	40	2	AAQ94428	Human Rae
95	13	7.3	40	13	ADR50610	Adt50610 PCR prime
96	13	7.3	41	2	AAV47770	AAV47770 Maize pol
97	13	7.3	41	2	AAV47771	AAV47771 Maize pol
98	13	7.3	41	6	ABL40992	ABL40992 Homo DNA
99	13	7.3	41	6	ABZ45216	ABZ45216 Human ATP
100	13	7.3	41	6	ABZ49628	ABZ49628 Human snl

## ALIGNMENTS

## RESULT 1

AADS0042 standard; DNA; 32 BP.

AC AADS0042; (first entry)

DT 24-MAR-2003

Human flidnaMAPKAP-2 CDNA cloning PCR primer #5.

Human; mitogen-activated protein kinase activating protein kinase-2; MAPKAP-2 kinase; signal transduction; cell proliferative disorder; immune system disorder; inflammation; arthritis; immunomodulator; cytostatic; gene therapy; PCR; primer; ss.

Homo sapiens.

WO200230524-A2.

14-NOV-2002.

25-FEB-2002; 2002WO-US005670.

28-FEB-2001; 2001US-0272260P.

(MERI) MERCK &amp; CO INC.

Lograsso P, Hawkins J, Lisnack JM;

WPI; 2003-111970/10.

New isolated nucleic acid molecule encoding a human mitogen-activated protein kinase activating protein kinase-2 (MAPKAP-2), useful for treating immune-system related disorders, inflammation and arthritis.

Example 1; Page 124; 150pp; English.

The invention relates to an isolated nucleic acid molecule comprising a sequence of nucleotides that encode a human mitogen-activated protein kinase activating protein kinase-2 (MAPKAP-2 kinase) and a coding region that encodes a splice variant of a MAPKAP-2 kinase. The invention is especially useful in regulating signal transduction in a cell and in diagnosing or treating MAPKAP-2-mediated disorders eg. cell proliferative disorders, immune system disorders, inflammation, arthritis. The nucleic acid and the polypeptide may also be used in screening assays, predictive medicine, diagnostic or prognostic assays, chromosome mapping, tissue typing, pharmacogenomics and in monitoring clinical trials. The invention is useful in gene therapy. The present sequence is human full length MAPKAP-2 kinase, flidnaMAPKAP-2 CDNA cloning PCR primer

Sequence 32 BP; 5 A; 15 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 9.0%; Score 16; DB 8; Length 32;

Best Local Similarity 100.0%; Pred. No. 9.9e+02; Mismatches 0; Indels 0; Gaps 0;

122 CCCCTCCGAGGCGCAG 137

10 CCCCTCCGAGGCGCAG 25

## RESULT 2

ABX10978/c standard; DNA; 18 BP.

ABX10978; (first entry)

Human Zepmol gene specific PCR primer ZC17, 822.

Human; PCR; ss; Zepmol; epithelial morphogenesis; dermatological; vulnary; endocrine; gene therapy; protein transport; primer; neurotransmission; epithelial morphogenesis; epithelial cell disorder; alopecia; chromosomal mapping.

Homo sapiens.

US2003032778-A1.

13-FEB-2003.

26-FEB-2002; 2002US-00085188.

14-DEC-1998; 98US-0112246P.

13-DEC-1999; 99US-00459544.

(ZYMO) ZYMOGENETICS INC.

Presnell SR, Taft DW;

WPI; 2003-466250/44.

New isolated polypeptide from the human syntaxin/epimorphin family, designated as Zepmol, useful in protein transport, neurotransmission, and epithelial morphogenesis for treating epithelial cell disorders, such as alopecia.

Example 2; Page 33; 39pp; English.

This invention relates to a novel polypeptide, designated Zepmol which is capable of effecting epithelial morphogenesis. The invention also comprises an expression vector comprising the Zepmol nucleic acid molecule, a method for producing the human Zepmol protein of the invention and a method for detecting the presence of Zepmol or Zepmol RNA in a biological sample. The DNA and protein sequences of the invention may have dermatological, vulnary or endocrine activities and may be used in gene therapy. The polypeptides, nucleic acid molecules and methods of the invention are useful in protein transport, neurotransmission, and epithelial morphogenesis, particularly for treating epithelial cell disorders, such as alopecia. The present sequence represents a PCR primer specific for the human Zepmol DNA sequence of the invention, this PCR primer was used with the primer shown in ABX10979 to map the chromosomal location of the human Zepmol gene

Sequence 18 BP; 2 A; 2 C; 10 G; 4 T; 0 U; 0 Other;

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Best Local Similarity 100.0%; Pred. No. 3.1e+03; Mismatches 0; Indels 0; Gaps 0;

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122 CCCCTCCGAGGCGCAG 137

10 CCCCTCCGAGGCGCAG 25

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 1086.04 Seconds  
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Gapop 60.0 , Gapext 60.0

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Word size : 0

Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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DEFINITION Sequence 399 from Patent EP1281758.  
ACCESSION AX687667  
VERSION AX687667.1 GI:29410363  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 399 05-FEB-2003;  
Aeomica, Inc. (US)  
LOCATION/Qualifiers

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ACCESSION AX687668  
VERSION AX687668.1 GI:29410364  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 400 05-FEB-2003;  
Aeomica, Inc. (US)  
LOCATION/Qualifiers

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DEFINITION Sequence 401 from Patent EP1281758.  
ACCESSION AX687669  
VERSION AX687669.1 GI:29410365  
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 401 05-FEB-2003;  
Aeomica, Inc. (US)  
LOCATION/Qualifiers

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DEFINITION Sequence 402 from Patent EP1281758.  
ACCESSION AX687670  
VERSION AX687670.1 GI:29410366  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
AUTHORS Shannon, M., Gu, Y. and Nguyen, C.T.  
TITLE Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and mdz12  
JOURNAL Patent: EP 1281758-A 402 05-FEB-2003;  
Aeomica, Inc. (US)  
LOCATION/Qualifiers

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QY 19 TTCTCTCACTATCCT 32  
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Db 1 TTCTCTCACTATCCT 14

## RESULT 5

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 8, 2005, 04:55:56 ; Search time 472.914 Seconds  
(without alignments)  
4536.068 Million cell updates/sec

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Gapop 60.0, Gapext 60.0

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Total number of hits satisfying chosen parameters: 10399348

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Pred. No. is the number of results predicted by chance to have a  
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## SUMMARIES

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C	92	17	5.5	42	22	US-10-500-361A-100	Sequence 100, App
C	93	17	5.5	43	9	US-09-179-536B-191	Sequence 191, App
C	94	17	5.5	43	10	US-09-297-576A-191	Sequence 191, App
C	95	17	5.5	44	9	US-09-179-536B-192	Sequence 192, App
C	96	17	5.5	44	10	US-09-297-576A-192	Sequence 192, App
C	97	17	5.5	45	9	US-09-179-536B-193	Sequence 193, App
C	98	17	5.5	45	10	US-09-297-576A-193	Sequence 193, App
C	99	17	5.5	46	9	US-09-179-536B-194	Sequence 194, App
C	100	17	5.5	46	10	US-09-297-576A-194	Sequence 194, App

## ALIGNMENTS

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RESULT 1
US-10-956-157-206499/c
; Sequence 206499, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 206499
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
; US-10-956-157-206499

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Query Match 8.1%; Score 25; DB 21; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.0024;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 150 GGCTACGATAGTACGATGACGGGC 174  
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db 25 GGCTACGATAGTACGATGACGGGC 1

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RESULT 2
US-10-956-157-214615/c
; Sequence 214615, Application US/10956157
; Publication No. US20050118625A1
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; GENERAL INFORMATION:
;
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
;
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
;
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 214615
;
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Probe Sequence
;
US-10-956-157-214615

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Query Match	8.1%;	Score 25;	DB 21;	Length 25;
Best Local Similarity	100.0%;	Pred. No. 0.0024;		
Matches 25;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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QY      203 GCAAGTGTCCAGCTGCTGCACTGC 227
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Db      25  GCAAGTGTCCAGCTGCTGCACTGC 1

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RESULT 3
US-10-956-157-201630/c
: Sequence 201630, 'Application US/10956157
: Publication No.' US20050118625A1
: GENERAL INFORMATION:
: APPLICANT: Wyeth
: APPLICANT: Mounes, William
: TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
: TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
: FILE REFERENCE: 031896-043000 (AM 101081)
: CURRENT APPLICATION NUMBER: US/10/956,157
: CURRENT FILING DATE: 2004-10-04
: NUMBER OF SEQ ID NOS: 319805
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 201630
: LENGTH: 25
: TYPE: DNA
: ORGANISM: Probe Sequence
: US-10-956-157-201630

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	Query Match	7.5%; Score 23; DB 21;	Length 25;
	Best Local Similarity	100.0%; Pred. No. 0.032;	
	Matches 23; Conservative 0;	Mismatches 0;	Indels 0; Gaps 0.
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Dδ	23 ACCAGACCAATTCAGCGGTGG	1	

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RESULT 4
US-11-036-317-214871/c
: Sequence 214871, Application US/11036317
: Publication No. US2005021483A1
GENERAL INFORMATION:
APPLICANT: Williams, Alan
APPLICANT: Blume, John
: TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
: FILE REFERENCE: 3654.1
: CURRENT APPLICATION NUMBER: US/11/036,317
: CURRENT FILING DATE: 2005-01-13
: PRIOR APPLICATION NUMBER: US 60/536,639
: PRIOR FILING DATE: 2004-01-13
: NUMBER OF SEQ. ID NOS: 991174
: SOFTWARE: Microarray probe Sequence Listing Generator V 1.1
: SEQ. ID NO 214871
LENGTH: 25
: TYPE: DNA
: ORGANISM: Mus musculus
US-11-036-317-214871

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	Query Match	6.2%	Score 19;	DB 24;	Length 25;
	Best Local Similarity	100.0%	Pred. No. 5,7;		
	Matches 19;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
OY	176 GCACGACAGCAGCGCCAGCA	194			
Db	23 GCACGACAGCAGCGCCAGCA	5			

RESULT 5  
US-11-036-317-227382  
; Sequence 227382, Application US/11036317  
; Publication No. US20050214823A1

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 23:25:05 : Search time 94.5143 Seconds  
(without alignments)  
5352.244 Million cell updates/sec

Title: US-09-887-941B-2

Perfect score: 308  
Sequence: 1 ctacggtagctgctgctgctg.....ggacacacagatcgcgggggg 308

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database : Issued Patents NA:\*

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2: /cgm2\_6/ptodata/1/ina/5B.COMB.seq:\*  
3: /cgm2\_6/ptodata/1/ina/6A.COMB.seq:\*  
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5: /cgm2\_6/ptodata/1/ina/PCtUS.COMB.seq:\*  
6: /cgm2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	6.8	43	2	US-08-531-927B-17
C 2	20	6.5	33	5	PCT-US95-06385-7
C 3	17	5.5	18	2	US-08-863-639A-17
C 4	17	5.5	21	2	US-08-267-803B-66
C 5	17	5.5	21	2	US-08-863-639A-28
C 6	17	5.5	21	2	US-08-863-639A-40
C 7	17	5.5	21	2	US-08-863-639A-60
C 8	17	5.5	21	2	US-08-863-639A-66
C 9	17	5.5	21	2	US-08-863-639A-69
C 10	17	5.5	21	2	US-08-863-639A-87
C 11	17	5.5	24	2	US-08-863-639A-94
C 12	17	5.5	25	4	US-09-396-196G-74107
C 13	17	5.5	30	1	US-08-068-747-6
C 14	17	5.5	30	1	US-08-068-747-11
C 15	17	5.5	30	1	US-08-863-639A-30
C 16	17	5.5	30	3	US-09-135-994-4
C 17	17	5.5	30	4	US-09-684-843A-4
C 18	17	5.5	31	2	US-08-570-155-14
C 19	17	5.5	31	5	PCT-US95-02861-14
C 20	17	5.5	33	2	US-08-863-639A-29
C 21	17	5.5	33	4	US-09-475-947A-251
C 22	17	5.5	36	2	US-08-863-639A-31
C 23	17	5.5	40	4	US-09-703-498A-11
C 24	16	5.2	25	4	US-09-396-196G-50624
C 25	16	5.2	25	4	US-09-396-196G-115505
C 26	16	5.2	31	2	US-08-570-155-15
C 27	16	5.2	31	5	PCT-US95-02861-15

C 28	16	5.2	41	3	US-09-422-936-4	Sequence 4, Appli
C 29	16	5.2	43	3	US-08-732-708C-10	Sequence 10, Appli
C 30	16	5.2	50	3	US-09-422-936-6	Sequence 6, Appli
C 31	16	5.2	50	3	US-09-422-936-22	Sequence 22, Appli
C 32	16	5.2	50	3	US-09-422-936-62	Sequence 62, Appli
C 33	15	4.9	18	3	US-09-487-444-11	Sequence 11, Appli
C 34	15	4.9	21	3	US-08-628-540-8	Sequence 8, Appli
C 35	15	4.9	21	3	US-08-628-540-9	Sequence 9, Appli
C 36	15	4.9	21	3	US-08-941-100-3	Sequence 3, Appli
C 37	15	4.9	21	3	US-08-941-100-4	Sequence 4, Appli
C 38	15	4.9	25	4	US-09-396-196G-2490	Sequence 2490, Ap
C 39	15	4.9	25	4	US-09-396-196G-5126	Sequence 5126, Ap
C 40	15	4.9	25	4	US-09-396-196G-50623	Sequence 50623, A
C 41	15	4.9	25	4	US-09-396-196G-115504	Sequence 115504,
C 42	15	4.9	34	3	US-08-968-563-46	Sequence 46, Appli
C 43	15	4.9	34	3	US-08-968-563A-46	Sequence 46, Appli
C 44	15	4.9	34	3	US-09-297-928-18	Sequence 18, Appli
C 45	15	4.9	34	4	US-09-641-652-24	Sequence 24, Appli
C 46	15	4.9	39	2	US-08-533-298-16	Sequence 16, Appli
C 47	15	4.9	39	2	US-08-533-298-18	Sequence 18, Appli
C 48	15	4.9	39	3	US-08-721-458B-67	Sequence 67, Appli
C 49	15	4.9	41	3	US-08-721-458B-68	Sequence 68, Appli
C 50	15	4.9	45	3	US-08-721-458B-62	Sequence 62, Appli
C 51	15	4.9	47	3	US-09-641-638-877	Sequence 877, App
C 52	15	4.9	47	3	US-09-641-638-878	Sequence 877, App
C 53	15	4.9	47	4	US-10-170-097-877	Sequence 877, App
C 54	15	4.9	47	4	US-10-170-097-878	Sequence 878, App
C 55	14	4.5	15	3	US-09-163-485-13	Sequence 13, Appli
C 56	14	4.5	15	4	US-09-475-947A-304	Sequence 304, App
C 57	14	4.5	18	4	US-09-679-298A-30	Sequence 30, Appli
C 58	14	4.5	20	3	US-09-907-843-23	Sequence 23, Appli
C 59	14	4.5	23	4	US-09-083-268-11	Sequence 11, Appli
C 60	14	4.5	25	4	US-09-396-196G-51515	Sequence 51515, A
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C 66	14	4.5	25	4	US-09-396-196G-102989	Sequence 102989,
C 67	14	4.5	25	4	US-09-396-196G-102990	Sequence 102990,
C 68	14	4.5	25	4	US-09-396-196G-102991	Sequence 102991,
C 69	14	4.5	25	4	US-09-396-196G-125084	Sequence 125084,
C 70	14	4.5	32	1	US-08-053-867A-22	Sequence 22, Appli
C 71	14	4.5	35	4	US-09-598-747-32	Sequence 32, Appli
C 72	14	4.5	36	2	US-08-863-639A-18	Sequence 18, Appli
C 73	14	4.5	36	4	US-09-438-268-50	Sequence 50, Appli
C 74	14	4.5	38	2	US-08-857-946-108	Sequence 108, App
C 75	14	4.5	38	3	US-08-970-740-108	Sequence 108, App
C 76	14	4.5	39	3	US-08-444-818-761	Sequence 761, App
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C 78	14	4.5	47	3	US-09-641-638-876	Sequence 876, App
C 79	14	4.5	47	4	US-10-170-097-876	Sequence 876, App
C 80	13	4.2	15	3	US-09-180-437-104	Sequence 104, App
C 81	13	4.2	18	3	US-09-255-911-31	Sequence 31, Appli
C 82	13	4.2	19	4	US-09-422-978-4399	Sequence 4399, Ap
C 83	13	4.2	20	3	US-09-288-461-27	Sequence 27, Appli
C 84	13	4.2	20	4	US-09-758-881-27	Sequence 27, Appli
C 85	13	4.2	20	4	US-09-899-440-3	Sequence 3, Appli
C 86	13	4.2	22	4	US-09-390-134B-13	Sequence 13, Appli
C 87	13	4.2	23	3	US-09-632-098-24	Sequence 24, Appli
C 88	13	4.2	23	4	US-10-177-308-24	Sequence 24, Appli
C 89	13	4.2	25	4	US-09-396-196G-7992	Sequence 7992, Ap
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C 91	13	4.2	25	4	US-09-396-196G-16881	Sequence 16881, A
C 92	13	4.2	25	4	US-09-396-196G-18819	Sequence 18819, A
C 93	13	4.2	25	4	US-09-396-196G-22097	Sequence 22097, A
C 94	13	4.2	25	4	US-09-396-196G-22098	Sequence 22098, A
C 95	13	4.2	25	4	US-09-396-196G-23457	Sequence 23457, A
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C 99	13	4.2	25	4	US-09-396-196G-72670	Sequence 72670, A
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## ALIGNMENTS

RESULT 1  
US-08-531-927B-17/C  
Sequence 17, Application US/08531927B  
Patent No. 5840491  
GENERAL INFORMATION:  
APPLICANT: Kakizuka, Akira  
TITLE OF INVENTION: DNA Sequence Encoding the Machado-Joseph  
Patent No. 5840491  
TITLE OF INVENTION: Disease Gene and Uses Thereof  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Millitia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173-4799  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/531,927B  
FILING DATE: 21-SEP-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP H6-251600  
FILING DATE: 21-SEP-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: ATH95-01A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 43 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-531-927B-17

Query Match 6.8%; Score 21; DB 2; Length 43;  
Best Local Similarity 100.0%; Pred. No. 0.63;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 CAGCAGCAGCAGCAGCAGCA 194  
DB 42 CAGCAGCAGCAGCAGCAGCA 22

RESULT 2  
PCT-US95-06385-7/C  
Sequence 7, Application PC/TUS9506385  
GENERAL INFORMATION:  
APPLICANT: Wei, ET AL.  
TITLE OF INVENTION: Transforming Growth Factor Alpha III  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESS: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA

ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/06385  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: NONE  
FILING DATE: NONE  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-351  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1740  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: Oligonucleotide  
PCT-US95-06385-7

Query Match 6.5%; Score 20; DB 5; Length 33;  
Best Local Similarity 100.0%; Pred. No. 2;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 150 GGCTACGATGAGTAGCATGA 169  
DB 33 GGCTACGATGAGTAGCATGA 14

RESULT 3  
US-08-863-639A-17/C  
Sequence 17, Application US/08863639A  
Patent No. 5981185  
GENERAL INFORMATION:  
APPLICANT: Matson, Robert S.  
APPLICANT: Coassin, Peter J.  
APPLICANT: Rampal, Jang B.  
APPLICANT: Caskey, C.T.  
TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS  
NUMBER OF SEQUENCES: 95  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, 9th Floor  
CITY: Pasadena  
STATE: CA  
COUNTRY: USA  
ZIP: 91101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: Windows 95  
SOFTWARE: Corel wordperfect 8 version  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/863,639A  
FILING DATE: May 28, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Joseph E. Mueh  
REGISTRATION NUMBER: 20,532  
REFERENCE/DOCKET NUMBER: 11859-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (626) 796-4000  
TELEFAX: (626) 795-6321  
INFORMATION FOR SEQ ID NO: 17:





88 11 3.6 25 9 CG715742 1119043B1  
99 11 3.6 25 9 CG724924 1119083B0  
c 100 11 3.6 26 5 B0584383 B0584383 E011859-0

## ALIGNMENTS

RESULT 1  
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DEFINITION mRNA sequence.  
ACCESSION BF537767  
VERSION BF537767.1 GI:11625135  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 50)  
NIH-MGC http://mgi.nci.nih.gov/  
National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaabs@mail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LMNL at:  
http://image.llnl.gov  
Plate: LM9526 row: c column: 17  
High quality sequence stop: 50.  
Location/Qualifiers  
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/clone="IMAGE:4193608"  
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/clone\_1lb="NCI CGAP SG2"  
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site: 1;  
NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo  
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Technologies. Note: this is a NCI\_CGAP Library."

## FEATURES

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/clone="IMAGE:4193608"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_1lb="NCI CGAP SG2"  
/note="Organ: salivary gland; Vector: pCMV-SPORT6; Site: 1;  
NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo  
dT. Average insert size 1.3 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

## ORIGIN

Query Match 5.8%; Score 18; DB 2; Length 50;  
Best Local Similarity 100.0%; Pred. No. 2.7e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 172 GCAGCAGCAGCAGCAGC 189  
Dd 30 GCAGCAGCAGCAGCAGC 13

RESULT 2  
A2779573 24 bp DNA linear GSS 16-FEB-2001  
LOCUS A2779573  
DEFINITION 2M0016K09 Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCG2M0016K09 F, genomic survey sequence.  
ACCESSION A2779573  
VERSION A2779573.1 GI:12910362  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 24)  
REFERENCE 1 (bases 1 to 24)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingy,A., von  
Niederhausen,A. and Wright,D., Weis,R.  
Mouse whole genome scaffolding with paired end reads from 10kb  
plasmid inserts  
Unpublished (2000)

## JOURNAL

CONTACT: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunne@genetics.utah.edu  
Insert length: 10000 Std Error: 0.00  
Plate: 0016 row: K column: 09  
Seq primer: CGTTGTAAACGACGCGCAGT  
Class: plasmid ends  
High quality sequence stop: 24.  
Location/Qualifiers  
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/strain="C57BL/6J"  
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/clone="UGCG2M0016K09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UGCGIM library"  
/note="Vector: pMD29v; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
was hydrodynamically sheared by repeated passage through a  
0.005 inch orifice at constant velocity. The sheared DNA  
was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
ligated to the blunt ends in high molar excess. The  
adapted DNA was purified and size-selected for a 9.5 to  
10.5 kb range using preparative agarose gel  
electrophoresis. Vector DNA was prepared from a derivative  
of pMD42 (GI:4732114|9b|AF129072.1), a copy-number  
inducible derivative of plasmid R1. The vector was ligated  
with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## FEATURES

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/organism="Mus musculus"  
/mol\_type="genomic DNA"  
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/clone="UGCG2M0016K09"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_1lb="Mouse 10kb plasmid UGCGIM library"  
/note="Vector: pMD29v; Purified genomic DNA from M.  
musculus C57BL/6J (male) was obtained from the Jackson  
Laboratory Mouse DNA Resource  
(http://www.jax.org/resources/documents/dnares/). The DNA  
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was blunt end-repaired with T4 DNA polymerase and T4  
polynucleotide kinase. Adaptor oligonucleotides were  
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of pMD42 (GI:4732114|9b|AF129072.1), a copy-number  
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with adaptors complementary to the insert adaptors and  
purified. The sheared, adapted mouse DNA was annealed to  
adapted vector DNA, and transformed into  
chemically-competent E. coli XL10-Gold (Stratagene) cells  
and selected for ampicillin resistance."

## ORIGIN

Query Match 5.5%; Score 17; DB 8; Length 24;  
Best Local Similarity 100.0%; Pred. No. 9.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 GCAGCAGCAGCAGCAGC 189  
Dd 1 GCAGCAGCAGCAGCAGC 17

RESULT 3  
A2404206/c 27 bp DNA linear GSS 03-OCT-2000  
LOCUS A2404206  
DEFINITION IM0172120F Mouse 10kb plasmid UGCGIM library Mus musculus genomic  
clone UGCGIM0172120 F, genomic survey sequence.  
ACCESSION A2404206  
VERSION A2404206.1 GI:10528219  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 27)  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 323.886 Seconds  
(without alignments)  
5629.394 Million cell updates/sec

Title: US-09-887-941B-2

Perfect score: 308  
Sequence: 1 ctagggttagctgctgctgctg.....ggaacacagatcgccggggg 308

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

1: Geneseq\_16Dec04:\*  
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3: geneseqn1990s:\*  
4: geneseqn2000s:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	6.5	33	2	AA15433 Human tra
2	19	6.2	31	3	AA289256 Human emb
3	19	6.2	36	6	ABA96943 Human den
4	19	6.2	38	4	AAH48359 Human FOA
5	19	6.2	45	5	AAH24422 Oligonuc
6	18	5.8	20	3	AAA55806 Human his
7	18	5.8	20	4	AAH43116 Antisense
8	18	5.8	20	4	AAH43116 Antisense
9	18	5.8	20	4	AAH43116 Antisense
10	18	5.8	20	4	AAH43116 Antisense
11	18	5.8	20	11	ABD22298 Human HDA
12	18	5.8	22	4	AA564183 Human sta
13	18	5.8	22	4	AA564181 Human pro
14	18	5.8	22	5	ACA59989 Prostate
15	18	5.8	22	5	ACA59991 Prostate
16	18	5.8	22	8	ACC95718 Prostate
17	18	5.8	22	8	ACC95716 Prostate
18	18	5.8	22	10	ADB14387 Human pro
19	18	5.8	22	10	ADB14385 Human pro
20	18	5.8	22	10	ADG26801 Human pro

21	18	5.8	22	10	ADG26803	ADG26803 Human pro
22	18	5.8	30	4	AA289258	AA289258 Human emb
23	18	5.8	31	3	AA129930	AA129930 Human sin
24	18	5.8	39	2	AA185339	AA185339 Spider si
25	18	5.8	39	2	AA185336	AA185336 Spider si
26	18	5.8	39	2	AA185358	AA185358 Spider si
27	18	5.8	39	2	AA185357	AA185357 Spider si
28	18	5.8	44	2	AAV68379	AAV68379 Clone #5
29	18	5.8	50	2	AAV68378	AAV68378 Clone #4
30	18	5.5	18	4	AA13717	AA13717 Simple se
31	17	5.5	18	12	ADN97239	ADN97239 Primer of
32	17	5.5	18	12	ADN97239	ADN97239 Primer of
33	17	5.5	18	12	ADN97239	ADN97239 Primer of
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C 94      17      5.5      40      6      AAD33976 PCR prime
C 95      17      5.5      40      8      Abx97712 Human sec
C 96      17      5.5      40      8      ACA93223 Human sec
C 97      17      5.5      40      10     Adf73214 Paramyxov
          98      17      5.5      40      12     Adf55163 Solid sta
          99      17      5.5      41      2     AAV39671 Solid sta
          100     17      5.5      41      4     AbK98808 Solid sta
```

## ALIGNMENTS

```
RESULT 1
AAT45433/c
ID AAT45433 standard; cDNA; 33 BP.
```

```
AC AAT45433;
XX
XX 30-JUL-1997 (first entry)
```

```
DE Human transforming growth factor alpha HII PCR primer.
```

```
KW TGFalpha-HII; AIDS; dementia; ocular disease; kidney disorder;
KW liver disorder; hair follicle development; angiogenesis; ulcer;
KW corneal incision; embryogenesis; gene therapy; neoplasia; psoriasis;
KW polymerase chain reaction; ss.
```

```
OS Synthetic.
```

```
PN WO9636709-A1.
```

```
PD 21-NOV-1996.
```

```
XX 19-MAY-1995; 95WO-US006386.
```

```
PR 19-MAY-1995; 95WO-US006386.
```

```
XX (HUMA-) HUMAN GENOME SCI INC.
```

```
PI Wei Y, Meissner PS, Ni J;
```

```
XX WPI; 1997-012084/01.
```

```
PT Nucleic acid encoding human transforming growth factor-alpha HII - useful
PT for treating, e.g. ocular diseases, kidney and liver disorders, or to
PT stimulate wound healing etc.
```

```
PS Example 2; Page 40; 73pp; English.
```

```
CC The present sequence encodes the PCR primer for amplifying human
CC transforming growth factor alpha HII (TGFalpha-HII), the construct starts
CC at nucleotide 402 and ends at nucleotide 1248. Human TGFalpha-HII can be
CC used to stimulate wound healing; to restore normal neurological
CC functioning after trauma or AIDS; dementia; to treat ocular diseases,
CC kidney and liver disorders; promote hair follicle development; to
CC stimulate angiogenesis for treating burns, ulcers, corneal incisions; and
CC to stimulate embryogenesis. The TGFalpha-HII can be used directly or is
CC generated in situ, i.e. by gene therapy. Antagonists of TGFalpha-HII are
CC useful for treating neoplasia and for treating certain skin disorders,
CC such as psoriasis. Detecting mutations in the polynucleotide sequence is
CC used for diagnosing diseases (or susceptibility to diseases) which result
CC from underexpression of TGFalpha-HII
```

```
XX Sequence 33 BP; 6 A; 13 C; 7 G; 7 T; 0 U; 0 Other;
```

```
Query Match 6.5%; Score 20; DB 2; Length 33;
```

```
Best Local Similarity 100.0%; Pred. No. 8.5;
```

```
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 150 GGCTACGATGAGTACATGA 169
DB 33 GGCTACGATGAGTACATGA 14
```

```
RESULT 2
AAZ89256/c
ID AAZ89256 standard; DNA; 31 BP.
```

```
AC AAZ89256;
```

```
XX 09-JUN-2000 (first entry)
```

```
DE Human embryonic brain protein PCR primer #1.
```

```
KW Human; brain; nerve degeneration; neurotropic; neuroprotective;
KW anticonvulsant; antiparkinsonian; antidiabetic; treatment; infarction;
KW Parkinson's disease; Alzheimer's disease; Huntington's disease;
KW muscular hypoplastic lateral sclerosis; diabetic neuropathy; PCR primer;
KW ss.
```

```
OS Homo sapiens.
```

```
PN WO200007614-A1.
```

```
PD 17-FEB-2000.
```

```
XX 02-AUG-1999; 99WO-JP004171.
```

```
PR 05-AUG-1998; 98JP-00221866.
```

```
PR 05-FEB-1999; 99JP-00029164.
```

```
XX (SAKA ) OTSUKA PHARM CO LTD.
```

```
PI Horie M, Hirano H, Kyushiki H, Mitsumoto Y, Mori A, Watanabe A;
```

```
XX WPI; 2000-205566/18.
```

```
PT New protein isolated from human embryonic brain useful for treating nerve
PT degeneration diseases e.g. Parkinson's diseases and Alzheimer's disease.
```

```
PS Example 2; Page 61; 69pp; Japanese.
```

```
CC This invention describes a novel human embryonic brain derived protein
CC (I) which has neurotropic, neuroprotective, anticonvulsant,
CC antiparkinsonian and antidiabetic activity. (I) is useful for treating
CC nerve degeneration diseases e.g. Parkinson's disease, Alzheimer's
CC disease, muscular hypoplastic lateral sclerosis, Huntington's disease,
CC brain infarction, diabetic neuropathy and traumatic nerve degeneration.
CC AAZ89256-289234 represent PCR primers used in the isolation and
CC amplification of the human brain protein described in the method of the
CC invention
```

```
XX Sequence 31 BP; 4 A; 11 C; 9 G; 7 T; 0 U; 0 Other;
```

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Best Local Similarity 100.0%; Pred. No. 27;
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 132 AGCGAGCTTCACCGGCGG 150
DB 28 AGCGAGCTTCACCGGCGG 10
```

```
RESULT 3
```

```
ABA96943/c
ID ABA96943 standard; DNA; 36 BP.
```

```
XX ABA96943;
```

```
XX 20-MAY-2002 (first entry)
```

```
DE Human dendritic cell membrane protein Siglec-9 sense RT-PCR primer.
```

```
KW Human; Siglec-9; membrane protein; dendritic cell; DC;
KW sialic acid binding immunoglobulin-like lectin 9; anti-Siglec-9 antibody;
KW cancer; vaccine; immunotherapy; reverse transcription-PCR; RT-PCR;
```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 1889.83 Seconds  
(without alignments)  
7697.122 Million cell updates/sec

Title: US-09-887-941B-2

Perfect score: 308  
Sequence: 1 ctgagggtagcgtcgtctctg.....ggacacagatcgcg9999 308

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

GenEmbl:\*  
1: gb\_ha:\*  
2: gb\_hctg:\*  
3: gb\_in:\*  
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5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_seq:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	21	6.8	43	6	AR059527 Sequence
C 2	19	6.2	31	6	E37925
C 3	19	6.2	36	6	BD095049 Antibody
C 4	19	6.2	45	6	E59414
C 5	18	5.8	20	6	BD244919
C 6	18	5.8	20	6	AX053082
C 7	18	5.8	20	6	AX053091
C 8	18	5.8	20	6	AX546302
C 9	18	5.8	20	6	AX546392
C 10	18	5.8	22	6	AX267961
C 11	18	5.8	22	6	AX267963
C 12	18	5.8	30	6	E37927
C 13	17	5.5	18	6	AR084528
C 14	17	5.5	18	6	AX598368
C 15	17	5.5	21	6	AR053160
C 16	17	5.5	21	6	AR084539
C 17	17	5.5	21	6	AR084551
C 18	17	5.5	21	6	AR084571
C 19	17	5.5	21	6	AR084577

C 20	17	5.5	21	6	AR084580	AR084580 Sequence
C 21	17	5.5	21	6	AR084598	AR084598 Sequence
C 22	17	5.5	21	6	AX104588	AX104588 Sequence
C 23	17	5.5	21	6	AX355212	AX355212 Sequence
C 24	17	5.5	21	6	AX547641	AX547641 Sequence
C 25	17	5.5	23	6	AX926737	AX926737 Sequence
C 26	17	5.5	24	6	AR084605	AR084605 Sequence
C 27	17	5.5	24	6	BD169605	BD169605 Novel G P
C 28	17	5.5	24	6	BD182475	BD182475 Screening
C 29	17	5.5	24	6	BD102725	BD102725 Ligand fo
C 30	17	5.5	25	6	A27143	A27143 Synthetic 1
C 31	17	5.5	25	6	A27144	A27144 Synthetic 1
C 32	17	5.5	30	6	AR084541	AR084541 Sequence
C 33	17	5.5	30	6	AR165925	AR165925 Sequence
C 34	17	5.5	30	6	E34522	E34522 SCA7 gene a
C 35	17	5.5	30	6	I84405	I84405 Sequence 6
C 36	17	5.5	30	6	I84410	I84410 Sequence 11
C 37	17	5.5	30	6	AX614111	AX614111 Sequence
C 38	17	5.5	31	6	AR078304	AR078304 Sequence
C 39	17	5.5	31	6	AR084540	AR084540 Sequence
C 40	17	5.5	33	6	BD177544	BD177544 Method fo
C 41	17	5.5	33	6	AR241963	AR241963 Sequence
C 42	17	5.5	36	6	A62704	A62704 Sequence 5
C 43	17	5.5	36	6	AR084542	AR084542 Sequence
C 44	17	5.5	37	6	AX328688	AX328688 Sequence
C 45	17	5.5	37	6	BD132253	BD132253 DNA diagn
C 46	17	5.5	38	6	AX328689	AX328689 Sequence
C 47	17	5.5	38	6	BD132254	BD132254 DNA diagn
C 48	17	5.5	39	6	AX328690	AX328690 Sequence
C 49	17	5.5	39	6	BD132255	BD132255 DNA diagn
C 50	17	5.5	40	6	BD175941	BD175941 Paromyxov
C 51	17	5.5	40	6	AR544634	AR544634 Sequence
C 52	17	5.5	40	6	AX328691	AX328691 Sequence
C 53	17	5.5	40	6	BD011782	BD011782 RNP deriv
C 54	17	5.5	40	6	BD132256	BD132256 DNA diagn
C 55	17	5.5	41	6	AX328692	AX328692 Sequence
C 56	17	5.5	41	6	BD132257	BD132257 DNA diagn
C 57	17	5.5	42	6	A62705	A62705 Sequence 6
C 58	17	5.5	42	6	AX328693	AX328693 Sequence
C 59	17	5.5	42	6	BD132258	BD132258 DNA diagn
C 60	17	5.5	43	6	AX328694	AX328694 Sequence
C 61	17	5.5	43	6	BD132259	BD132259 DNA diagn
C 62	17	5.5	44	6	AX328695	AX328695 Sequence
C 63	17	5.5	44	6	BD132260	BD132260 DNA diagn
C 64	17	5.5	45	6	AX328696	AX328696 Sequence
C 65	17	5.5	45	6	BD132261	BD132261 DNA diagn
C 66	17	5.5	46	6	AX328697	AX328697 Sequence
C 67	17	5.5	46	6	BD132262	BD132262 DNA diagn
C 68	17	5.5	47	6	AX328698	AX328698 Sequence
C 69	17	5.5	47	6	BD132263	BD132263 DNA diagn
C 70	17	5.5	48	6	AX328699	AX328699 Sequence
C 71	17	5.5	48	6	BD132264	BD132264 DNA diagn
C 72	17	5.5	49	6	AX167839	AX167839 Sequence
C 73	17	5.5	49	6	AX328700	AX328700 Sequence
C 74	17	5.5	49	6	BD132265	BD132265 DNA diagn
C 75	17	5.5	50	6	C0008695	C0008695 Sequence
C 76	17	5.5	50	6	AX164884	AX164884 Sequence
C 77	17	5.5	50	6	AX190222	AX190222 Sequence
C 78	17	5.5	50	6	AX328701	AX328701 Sequence
C 79	17	5.5	50	6	BD132266	BD132266 DNA diagn
C 80	17	5.5	20	6	AX053083	AX053083 Sequence
C 81	16	5.2	20	6	AX053092	AX053092 Sequence
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C 83	16	5.2	20	6	AX546303	AX546303 Sequence
C 84	16	5.2	20	6	AX546393	AX546393 Sequence
C 85	16	5.2	22	6	AX360164	AX360164 Sequence
C 86	16	5.2	23	6	AX767321	AX767321 Sequence
C 87	16	5.2	31	6	AR078305	AR078305 Sequence
C 88	16	5.2	34	6	AX328685	AX328685 Sequence
C 89	16	5.2	34	6	BD132250	BD132250 DNA diagn
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 C 94 16 5.2 38 6 AX054682 Sequence  
 C 95 16 5.2 38 6 BD124121 Novel GAB  
 C 96 16 5.2 41 6 AR236558 Sequence  
 C 97 16 5.2 43 6 AR11859 Sequence  
 C 98 16 5.2 43 6 BD132486 Binding m  
 C 99 16 5.2 50 6 AR236560 Sequence  
 C 100 16 5.2 50 6 AR236576 Sequence

## ALIGNMENTS

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 LOCUS AR059527/c 43 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 17 from patent US 5840491.  
 ACCESSION AR059527  
 VERSION AR059527.1 GI:5985977  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 43)  
 AUTHORS Kakiyuka, A.  
 TITLE DNA sequence encoding the Machado-Joseph disease gene and uses thereof  
 JOURNAL Patent: US 5840491-A 17 24-NOV-1998;  
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QY 174 CAGCAGCAGCAGCAGCAGCA 194  
 DB 42 CAGCAGCAGCAGCAGCAGCA 22

RESULT 2  
 LOCUS E37925/c 31 bp DNA linear PAT 31-JAN-2002  
 DEFINITION Remedy for diseases with nerve degeneration.  
 ACCESSION E37925  
 VERSION E37925.1 GI:18624860  
 KEYWORDS JP 2000109433-A/3.  
 SOURCE JP 2000109433-A/3.  
 ORGANISM synthetic construct  
 REFERENCE 1 (bases 1 to 31)  
 AUTHORS Horie, M., Hirano, N., Kyushiki, H., Mitsumoto, Y., Mori, A. and Watabe, A.  
 TITLE Remedy for diseases with nerve degeneration  
 JOURNAL Patent: JP 2000109433-A 3 18-APR-2000;  
 COMMENT OTSUKA PHARMACEUT CO LTD  
 OS Artificial Sequence  
 PN JP 2000109433-A/3  
 PD 18-APR-2000  
 PF 05-FEB-1999 JP 1999029164  
 PR MASATO HORIE, NAONOBU HIRANO, HIROYUKI KYUSHIKI, PI YASUHIRO MITSUMOTO,  
 PI ATSUSHI MORI, AKIHITO WATABE  
 PC A61K38/00, A61K31/00, A61K31/00, C07K14/52//C12N15/09,  
 PC A61K37/02,  
 PC C12N15/00  
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QY 132 AGCGAGCTTCAACCGGCGG 150  
 DB 28 AGCGAGCTTCAACCGGCGG 10

RESULT 3  
 LOCUS BD095049/c 36 bp DNA linear PAT 27-AUG-2002  
 DEFINITION Antibody against dendritic cell (DC) membrane molecule, Siglec-9, and DC detection method and DC separation method using it.  
 ACCESSION BD095049  
 VERSION BD095049.1 GI:22640637  
 KEYWORDS JP 2001352977-A/2.  
 SOURCE JP 2001352977-A/2.  
 ORGANISM synthetic construct  
 REFERENCE 1 (bases 1 to 36)  
 AUTHORS Watarai, H. and Yamaguchi, Y.  
 TITLE Antibody against dendritic cell (DC) membrane molecule, Siglec-9, and DC detection method and DC separation method using it  
 JOURNAL Patent: JP 2001352977-A 2 25-DEC-2001;  
 KIRIN BREWERY CO LTD

COMMENT OS Artificial Sequence  
 PN JP 2001352977-A/2  
 PD 25-DEC-2001  
 PF 12-JUN-2000 JP 2000176187  
 PI HIROSHI WATARAI, YASUNORI YAMAGUCHI  
 PC C12N15/02, C07K16/18, C12N15/09, C12P21/08, C12Q1/02, G01N33/53, PC G01N33/53

PC GOIN33/57//C12Q1/68, C12N15/00, C12N15/00  
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 CC sequence of Siglec-9 gene  
 CC key Location/Qualifiers  
 FT source 1..36  
 FT Location/Qualifiers  
 1..36  
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FEATURES  
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## ORIGIN

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RESULT 4  
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 DEFINITION Signal peptide.  
 ACCESSION E59414  
 VERSION E59414.1 GI:18622547  
 KEYWORDS JP 2000354490-A/1.  
 SOURCE JP 2000354490-A/1.  
 ORGANISM synthetic construct

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw.model

Run on: October 8, 2005, 04:55:56 : Search time 813.781 Seconds  
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Searched: 8443130 seqs, 3482420727 residues

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Published Applications NA.\*  
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and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	17	3.2	25	24	US-11-036-317-79000
5	17	3.2	25	24	US-11-036-317-101784
6	16	3.0	24	17	US-10-401-194-42
7	16	3.0	22	22	US-10-719-956-439303

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C	11	16	3.0	25	24	US-11-036-317-674408	Sequence 674408,
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C	13	16	3.0	25	24	US-11-036-317-807089	Sequence 807089,
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C	16	15	2.8	20	21	US-10-831-901A-13046	Sequence 13046, A
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C	18	15	2.8	20	21	US-10-831-901A-13048	Sequence 13048, A
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C	24	15	2.8	25	21	US-10-719-900-172532	Sequence 172532,
C	25	15	2.8	25	21	US-10-719-900-318333	Sequence 318333,
C	26	15	2.8	25	21	US-10-719-900-489619	Sequence 489619,
C	27	15	2.8	25	21	US-10-719-900-693095	Sequence 693095,
C	28	15	2.8	25	21	US-10-719-900-710757	Sequence 710757,
C	29	15	2.8	25	21	US-10-719-900-806438	Sequence 806438,
C	30	15	2.8	25	21	US-10-719-900-827771	Sequence 827771,
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C	33	15	2.8	25	21	US-10-809-189-68144	Sequence 68144, A
C	34	15	2.8	25	21	US-10-956-157-226091	Sequence 226091, A
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C	48	15	2.8	25	24	US-11-036-317-39247	Sequence 39247, A
C	49	15	2.8	25	24	US-11-036-317-104500	Sequence 104500,
C	50	15	2.8	25	24	US-11-036-317-493757	Sequence 493757,
C	51	15	2.8	25	24	US-11-036-317-658319	Sequence 658319,
C	52	15	2.8	25	24	US-11-036-317-747349	Sequence 747349,
C	53	15	2.8	25	24	US-11-036-317-783939	Sequence 783939,
C	54	15	2.8	35	21	US-10-688-255-40	Sequence 40, App1
C	55	15	2.8	47	16	US-10-211-160-25	Sequence 25, App1
C	56	15	2.8	47	16	US-10-051-681A-25	Sequence 25, App1
C	57	15	2.8	19	10	US-09-771-933-178	Sequence 178, App
C	58	15	2.6	19	10	US-10-871-222-319	Sequence 319, App
C	59	14	2.6	19	21	US-10-871-222-423	Sequence 423, App
C	60	14	2.6	19	21	US-10-923-142-98	Sequence 98, App1
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C	65	14	2.6	21	15	US-10-002-623-214	Sequence 214, App1
C	66	14	2.6	21	15	US-10-002-623-217	Sequence 217, App1
C	67	14	2.6	21	15	US-10-493-836-29	Sequence 29, App1
C	68	14	2.6	22	22	US-10-984-819-9	Sequence 9, App1
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C	71	14	2.6	25	15	US-10-098-263B-62446	Sequence 62446, A
C	72	14	2.6	25	15	US-10-098-263B-93196	Sequence 93196, A
C	73	14	2.6	25	15	US-10-098-263B-93196	Sequence 93196, A
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## ALIGNMENTS

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; GENERAL INFORMATION:
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; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
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; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
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; CURRENT FILING DATE: 2003-11-20
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; PRIOR APPLICATION NUMBER: 60/427,808
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; PRIOR FILING DATE: 2002 11 20
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; NUMBER OF SEQ ID NOS: 982914
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; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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; SEQ ID NO 844308
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; LENGTH: 25
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; TYPE: DNA
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; ORGANISM: Mus musculus
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US-10-719-900-844308
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## RESULT 2

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US-10-188-646-20
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; Sequence 20, Application US/10188646
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; Publication No. US20040005565A1
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; GENERAL INFORMATION:
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```
; APPLICANT: C. Frank Bennett
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```
; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
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; FILE REFERENCE: RTS-0373
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; CURRENT APPLICATION NUMBER: US/10/188,646
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; CURRENT FILING DATE: 2002-07-02
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; NUMBER OF SEQ ID NOS: 153
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; SEQ ID NO 20
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; LENGTH: 20
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; TYPE: DNA
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; ORGANISM: Artificial Sequence
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; FEATURE:
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; OTHER INFORMATION: Antisense Oligonucleotide
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US-10-188-646-20
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Db 1 AAGTGCAGAGCTGGGA 17
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## RESULT 3

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US-10-188-646-97/c
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; Sequence 97, Application US/10188646
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; Publication No. US20040005565A1
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; GENERAL INFORMATION:
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; APPLICANT: C. Frank Bennett
```

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; TITLE OF INVENTION: ANTISENSE MODULATION OF LIVIN EXPRESSION
```

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; FILE REFERENCE: RTS-0373
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; CURRENT APPLICATION NUMBER: US/10/188,646
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; CURRENT FILING DATE: 2002-07-02
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; LENGTH: 20
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; TYPE: DNA
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; ORGANISM: H. sapiens
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US-10-188-646-97
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## RESULT 4

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; Sequence 79000, Application US/11036317
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; Publication No. US20050214823A1
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; GENERAL INFORMATION:
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; APPLICANT: Williams, Alan
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; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
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; FILE REFERENCE: 3654.1
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; CURRENT APPLICATION NUMBER: US/11/036,317
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; CURRENT FILING DATE: 2005-01-13
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; PRIOR APPLICATION NUMBER: US 60/536,639
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; PRIOR FILING DATE: 2004-01-13
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; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
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; SEQ ID NO 79000
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; LENGTH: 25
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; TYPE: DNA
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; ORGANISM: Mus musculus
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US-11-036-317-79000
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Best Local Similarity 100.0%; Pred. No. 2e+02;
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Db 23 TGGCAGAGCTGGGATTC 7
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## RESULT 5

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; Sequence 101784, Application US/11036317
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; Publication No. US20050214823A1
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; GENERAL INFORMATION:
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Title: US-09-887-941b-1

Perfect score: 530

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Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1209694

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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2	16	3.0	47	US-10-170-097-853	Sequence 853, App
3	15	2.8	25	US-09-396-196G-56102	Sequence 56102, A
4	15	2.8	25	US-09-396-196G-68144	Sequence 68144, A
5	15	2.8	41	US-08-857-946-92	Sequence 92, App
6	15	2.8	41	US-08-970-740-92	Sequence 92, App
7	14	2.6	15	US-08-363-240A-117	Sequence 117, App
8	14	2.6	21	US-08-255-892-68	Sequence 68, App
9	14	2.6	25	US-09-396-196G-94424	Sequence 94424, A
10	14	2.6	25	US-09-396-196G-94425	Sequence 94425, A
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14	14	2.6	27	US-08-435-634-18	Sequence 18, App
15	14	2.6	27	US-09-011-336-39	Sequence 39, App
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C 33	13	2.5	18	4	US-09-934-035-1	Sequence 1, App
C 34	13	2.5	18	4	US-09-934-035-2	Sequence 2, App
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C 66	13	2.5	25	3	US-09-021-701-25	Sequence 25, App
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C 71	13	2.5	25	3	US-09-021-701-30	Sequence 30, App
C 72	13	2.5	25	4	US-09-827-998-1610	Sequence 1610, App
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C 74	13	2.5	25	4	US-09-827-998-1612	Sequence 1612, App
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C 80	13	2.5	25	4	US-09-827-998-1618	Sequence 1618, App
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C 100	13	2.5	26	4	US-09-640-419C-16	Sequence 16, App



## ALIGNMENTS

## RESULT 1

US-09-641-638-853/C  
Sequence 853, Application US/09641638  
Patent No. 6432648  
GENERAL INFORMATION:  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bougueleret, Lydie  
APPLICANT: Chumakov, Ilya  
APPLICANT: Cohen, Annick  
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
FILE REFERENCE: GENSET.051CPI  
CURRENT APPLICATION NUMBER: US/09/641,638  
CURRENT FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: US 09/502,330  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US 09/275,267  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/119,917  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 1304  
SOFTWARE: Patent.pm  
SEQ ID NO 853  
LENGTH: 47  
TYPE: DNA  
ORGANISM: Homo Sapiens  
FEATURE:  
NAME/KEY: allele  
LOCATION: 24  
OTHER INFORMATION: 12-529-376 : polymorphic base T or C  
US-09-641-638-853

## Query Match

Best Local Similarity 3.0%; Score 16; DB 3; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 171 CTCACAGAAAAGAG 186

DB 17 CTCACAGAAAAGAG 2

## RESULT 2

US-10-170-097-853/C  
Sequence 853, Application US/10170097  
Patent No. 6794143  
GENERAL INFORMATION:  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bougueleret, Lydie  
APPLICANT: Chumakov, Ilya  
APPLICANT: Cohen, Annick  
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
FILE REFERENCE: GEN-T114XC2D1  
CURRENT APPLICATION NUMBER: US/10/170,097  
CURRENT FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: US 09/641,638  
PRIOR FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: US 09/502,330  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US 09/275,267  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/119,917  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 1304

SOFTWARE: Patent.pm

SEQ ID NO 853

LENGTH: 47

TYPE: DNA

ORGANISM: Homo Sapiens

FEATURE:

NAME/KEY: allele

LOCATION: 24

OTHER INFORMATION: 12-529-376 : polymorphic base T or C

US-10-170-097-853

## Query Match

Best Local Similarity 3.0%; Score 16; DB 4; Length 47;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 17 CTCACAGAAAAGAG 2

## RESULT 3

US-09-396-196G-56102  
Sequence 56102, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 56102  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus  
US-09-396-196G-56102

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Best Local Similarity 100.0%; Pred. No. 6.9e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 9 GGAGGGCACTCAGA 23

## RESULT 4

US-09-396-196G-68144/C  
Sequence 68144, Application US/09396196G  
Patent No. 6821724  
GENERAL INFORMATION:  
APPLICANT: Michael Miltmann  
APPLICANT: David Lockhart  
APPLICANT: Affymetrix, Inc.  
TITLE OF INVENTION: Methods of Genetic Analysis  
FILE REFERENCE: 3101.1  
CURRENT APPLICATION NUMBER: US/09/396,196G  
CURRENT FILING DATE: 1999-09-15  
PRIOR APPLICATION NUMBER: 60/100,678  
PRIOR FILING DATE: 1998-09-17  
NUMBER OF SEQ ID NOS: 127806  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 68144  
LENGTH: 25  
TYPE: DNA  
ORGANISM: mus musculus

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Title: US-09-887-941B-1

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Gapop 60.0 , Gapept 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 159776

Minimum DB seq length: 0

Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

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6: gb\_est5:\*  
7: gb\_est6:\*  
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9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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                                ALIGNMENTS

RESULT 1
AUI04142      50 bp      mRNA      linear      EST 28-JAN-2004
LOCUS      AUI04142 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION      CA0A0007 mRNA sequence.
ACCESSION      AUI04142
VERSION      AUI04142.1 GI:13553663
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS      Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale
mapping of mRNA start sites
EMBO Rep. 2 (5), 388-393 (2001)
21270072
JOURNAL
MEDLINE
PUBMED
COMMENT      Contact: Yutaka Suzuki
Department of Virology
Institute of Medical Science, University of Tokyo
11375929
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yusuzuki@ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and
Sugano,S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997).

FEATURES
source
1..50
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="CA0A0007"
/clone_lib="Sugano Homo sapiens cDNA library"

ORIGIN

Query Match      3.0%; Score 16; DB 1; Length 50;
Best Local Similarity 100.0%; Pred. No. 4.5e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      460 GTGCTAGGCTGCAGAC 475
Db      35 GTGCTAGGCTGCAGAC 50

RESULT 2
A2964788      49 bp      DNA      linear      GSS 27-APR-2001
LOCUS      A2964788
DEFINITION      2M0234C1R Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0234C11 R, genomic survey sequence.
ACCESSION      A2964788
VERSION      A2964788.1 GI:13836015
KEYWORDS      GSS.
SOURCE      Mus musculus (house mouse)
ORGANISM      Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
AUTHORS      Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.

```

```

TITLE      Mouse whole genome scaffolding with paired end reads from 10kb
JOURNAL
COMMENT      plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0234 row: C column: 11
Seq primer: CACACGAGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 49.

FEATURES
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1..49
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0234C11"
/sex="Female"
/lab_host="E. coli strain XL10-Gold, TI-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC2M library"
/note="Vector: PMD42nv, Purified genomic DNA from M.
musculus C57BL/6J (female) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 [gi|4732114|gb|AF129072.1], a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

Query Match      2.6%; Score 14; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 5.7e+04;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      190 GTGAGAGACAGGAG 203
Db      16 GTGAGAGACAGGAG 29

RESULT 3
AUI04141      50 bp      mRNA      linear      EST 28-JAN-2004
LOCUS      AUI04141 Sugano Homo sapiens cDNA library Homo sapiens cDNA clone
DEFINITION      HEP15203, mRNA sequence.
ACCESSION      AUI04141
VERSION      AUI04141.1 GI:13553662
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS      Suzuki,Y., Taira,H., Tsunoda,T., Mizushima-Sugano,J., Sese,J.,
Hata,H., Ota,T., Isogai,T., Tanaka,T., Morishita,S., Okubo,K.,
Sakaki,Y., Nakamura,Y., Suyama,A. and Sugano,S.
Diverse transcriptional initiation revealed by fine, large-scale

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:29:11 ; Search time 557.336 Seconds  
(without alignments)  
5629.394 Million cell updates/sec

Title: US-09-887-941B-1

Perfect score: 530  
Sequence: 1 cccgcgacctaacgacgacga.....ggaacatttagagagcccta 530

Scoring table: OLIGO NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4167226

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

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1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	17	3.2	20	12	ADH89551		Adh89551 Human Liv
2	17	3.2	20	12	ADH89628		Adh89628 Human Liv
3	16	3.0	17	3	AAFO2256		Aafo2256 Hammethea
4	16	3.0	24	12	ADH56954		Adh56954 PCR prime
5	16	3.0	24	12	ADP48553		Adp48553 Chicken t
6	16	3.0	50	4	AA131874		Aa131874 Human SNP
7	15	2.8	25	13	ADBS31644		Adbs31644 Small int
8	15	2.8	28	12	AA180178		Aa180178 Primer #1
9	15	2.8	28	12	ADP81947		Adp81947 Human NR1
10	15	2.8	37	3	AAZ99008		Aaz99008 Slow upst
11	15	2.8	41	3	AAZ43351		Aaz43351 Murine Ty
12	15	2.8	41	3	AAA05336		Aaa05336 PCR prime
13	15	2.8	47	8	ABZ22300		Abz22300 Human D-a
14	15	2.8	47	9	AA160255		Aa160255 Human DAO
15	14	2.6	15	2	AA149758		Aa149758 Human CET
16	14	2.6	19	4	AAH28653		Aah28653 Human int
17	14	2.6	20	4	AAH89418		Aah89418 Sense PCR
18	14	2.6	20	4	AAH28654		Aah28654 Human int
19	14	2.6	20	10	ABZ88331		Abz88331 Human oli
20	14	2.6	20	10	ABZ88332		Abz88332 Human oli

21	14	2.6	20	11	ABD24561		Abd24561 A1652764-
22	14	2.6	20	11	ABD24562		Abd24562 A1652764-
23	14	2.6	21	2	AAQ20640		Aaq20640 Capture p
24	14	2.6	21	9	ACH03502		Ach03502 Human lat
25	14	2.6	21	11	ADM65058		Adm65058 Human y c
26	14	2.6	21	11	ADM65055		Adm65055 Human y c
27	14	2.6	22	8	ACC47855		Acc47855 Rat elast
28	14	2.6	22	2	AAV48420		Aav48420 Transform
29	14	2.6	24	3	AAH77032		Aah77032 Human NF-
30	14	2.6	24	4	AAH77032		Aah77032 Human NF-
31	14	2.6	25	9	AC112383		Ac112383 Human mic
32	14	2.6	25	9	AC162455		Ac162455 Human mic
33	14	2.6	25	9	AC163699		Ac163699 Human mic
34	14	2.6	25	9	AC193205		Ac193205 Human mic
35	14	2.6	25	9	AC193205		Ac193205 Human mic
36	14	2.6	27	2	AAQ57222		Aaq57222 Enzymatic
37	14	2.6	27	2	AAQ57222		Aaq57222 Enzymatic
38	14	2.6	27	2	AAQ57222		Aaq57222 Enzymatic
39	14	2.6	27	2	AAQ57222		Aaq57222 Enzymatic
40	14	2.6	27	2	AAQ57222		Aaq57222 Enzymatic
41	14	2.6	27	2	AAQ57222		Aaq57222 Enzymatic
42	14	2.6	27	2	AAQ57222		Aaq57222 Enzymatic
43	14	2.6	27	2	AAQ57222		Aaq57222 Enzymatic
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94	13	2.5	18	2	AAQ26546	AAQ26546 Control P
C	95	13	2.5	18	2	AAQ91959 T-cell R
C	96	13	2.5	18	2	AAQ92756 Vbeta20 T
C	97	13	2.5	18	2	AAQ94252 Primer JB
C	98	13	2.5	18	2	AAQ86621 Sonic hed
C	99	13	2.5	18	4	AAH23358 Nucleotid
C	100	13	2.5	18	6	AAH14344 3'-PCR pr

## ALIGNMENTS

## RESULT 1

ID ADH89551 standard; DNA; 20 BP.

ADH89551;

22-APR-2004 (first entry)

Human Livin antisense oligonucleotide ISIS 205802.

hyperproliferative disorder; aberrant apoptosis; human; ss; Livin; antisense.

Homo sapiens. Synthetic.

US2004005565-A1.

08-JAN-2004.

02-JUL-2002; 2002US-00188646.

02-JUL-2002; 2002US-00188646.

(ISIS-) ISIS PHARM INC.

Bennett CF, Dobie KW;

WPI; 2004-098436/10.

New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding Livin, useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis.

Example 15; SEQ ID NO 20; 60pp; English.

The invention relates to an antisense oligonucleotide targeted to a nucleic acid encoding Livin and that specifically hybridizes with the nucleic acid encoding Livin and inhibits expression of Livin. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis. The present sequence represents a human livin antisense oligonucleotide.

Sequence 20 BP; 5 A; 4 C; 8 G; 3 T; 0 U; 0 Other;

Query Match 3.2%; Score 17; DB 12; Length 20;

Best Local Similarity 100.0%; Pred. No. 3.7e+02; Mismatches 0; Indels 0; Gaps 0;

Oy	43	AAAGTGGCAGAGCTGGGA	59
Db	1	AAAGTGGCAGAGCTGGGA	17

## RESULT 2

ID ADH89628 standard; DNA; 20 BP.

ADH89628;

22-APR-2004 (first entry)

XX	XX	Human Livin target region ISIS 123462.
DE	DE	hyperproliferative disorder; aberrant apoptosis; human; ss; Livin.
XX	XX	Homo sapiens.
XX	XX	US2004005565-A1.
XX	XX	08-JAN-2004.
XX	XX	02-JUL-2002; 2002US-00188646.
XX	XX	02-JUL-2002; 2002US-00188646.
XX	XX	(ISIS-) ISIS PHARM INC.
XX	XX	Bennett CF, Dobie KW;
XX	XX	WPI; 2004-098436/10.
XX	XX	New antisense oligonucleotide, having a sequence targeted to a nucleic acid encoding Livin, useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis.
XX	XX	Example 15; SEQ ID NO 97; 60pp; English.
XX	XX	The invention relates to an antisense oligonucleotide targeted to a nucleic acid encoding Livin and that specifically hybridizes with the nucleic acid encoding Livin and inhibits expression of Livin. The antisense oligonucleotide is useful for preparing a composition for treating hyperproliferative disorder or aberrant apoptosis. The present sequence represents a human livin target region.
XX	XX	Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;
XX	XX	Query Match 3.2%; Score 17; DB 12; Length 20;
XX	XX	Best Local Similarity 100.0%; Pred. No. 3.7e+02; Mismatches 0; Indels 0; Gaps 0;

Oy	43	AAAGTGGCAGAGCTGGGA	59
Db	20	AAAGTGGCAGAGCTGGGA	4

## RESULT 3

ID AAF02256 standard; DNA; 17 BP.

AAF02256;

16-FEB-2001 (first entry)

Hammerhead ribozyme substrate #551.

Ribozyme; erythropoietin; granulocyte colony stimulating factor; interferon alpha; ss.

Homo sapiens.

WO200061729-A2.

19-OCT-2000.

11-APR-2000; 2000WO-US009721.

12-APR-1999; 99US-0129390P.

(RIBO-) RIBOZYME PHARM INC.

Blatt L, Zwick M, Pavco P, Mswiggen U;

WPI; 2000-647423/62.

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 7, 2005, 22:53:27 ; Search time 3251.98 Seconds  
(without alignments)  
7897.122 Million cell updates/sec

Title: US-09-887-941B-1  
Perfect score: 530  
Sequence: 1 cccgcgacctagagccagcga.....Ggaacatttagagcccta 530

Scoring table: OLIGO\_NUC  
Gapop 60.0, Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0  
Total number of hits satisfying chosen parameters: 1839042

Minimum DB seq length: 0  
Maximum DB seq length: 50

Post-processing: Listing first 100 summaries

Database :

GenEmbl:.\*  
1: gb\_ba:.\*  
2: gb\_hgt:.\*  
3: gb\_in:.\*  
4: gb\_om:.\*  
5: gb\_ov:.\*  
6: gb\_pat:.\*  
7: gb\_ph:.\*  
8: gb\_pl:.\*  
9: gb\_pr:.\*  
10: gb\_ro:.\*  
11: gb\_ste:.\*  
12: gb\_sy:.\*  
13: gb\_un:.\*  
14: gb\_vi:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16	3.0	17	6	BD254454
C 2	16	3.0	50	6	CO006442
C 3	15	2.8	28	6	CO866809
C 4	15	2.8	41	6	AR089810
C 5	15	2.8	45	9	HS4224269
C 6	15	2.8	47	6	AX741678
C 7	15	2.8	47	6	AX776500
C 8	14	2.6	21	6	A32743
C 9	14	2.6	21	6	I84297
C 10	14	2.6	23	6	A87861
C 11	14	2.6	23	6	A89828
C 12	14	2.6	23	6	BD065374
C 13	14	2.6	27	6	I37005
C 14	14	2.6	27	6	I93855
C 15	14	2.6	27	6	AR242663
C 16	14	2.6	27	6	AX317187
C 17	14	2.6	27	6	AX555913
C 18	14	2.6	31	6	I37152
C 19	14	2.6	31	6	I37153

C 20	14	2.6	31	6	I37154	I37154 Sequence 16
C 21	14	2.6	31	6	I94002	I94002 Sequence 16
C 22	14	2.6	31	6	I94003	I94003 Sequence 16
C 23	14	2.6	31	6	I94004	I94004 Sequence 16
C 24	14	2.6	35	6	CO814987	CO814987 Sequence
C 25	14	2.6	36	10	MMTCR48	MMTCR48 Sequence
C 26	14	2.6	50	6	CO858049	CO858049 Sequence
C 27	13	2.5	15	6	AR180156	AR180156 Sequence
C 28	13	2.5	16	6	A18727	A18727 kozak conse
C 29	13	2.5	17	6	AR434372	AR434372 Sequence
C 30	13	2.5	17	6	AR434373	AR434373 Sequence
C 31	13	2.5	17	6	AR434374	AR434374 Sequence
C 32	13	2.5	17	6	AR434375	AR434375 Sequence
C 33	13	2.5	17	6	AR434376	AR434376 Sequence
C 34	13	2.5	17	6	AX737603	AX737603 Sequence
C 35	13	2.5	18	6	A26383	A26383 probe no.1.
C 36	13	2.5	18	6	AR060406	AR060406 Sequence
C 37	13	2.5	18	6	AR128964	AR128964 Sequence
C 38	13	2.5	18	6	I65329	I65329 Sequence 51
C 39	13	2.5	18	6	AR534202	AR534202 Sequence
C 40	13	2.5	18	6	AR534203	AR534203 Sequence
C 41	13	2.5	18	6	AX202658	AX202658 Sequence
C 42	13	2.5	19	6	AR295829	AR295829 Sequence
C 43	13	2.5	19	6	AX394639	AX394639 Sequence
C 44	13	2.5	20	6	BD228522	BD228522 IL-17 hom
C 45	13	2.5	20	6	AR183227	AR183227 Sequence
C 46	13	2.5	20	6	AR234630	AR234630 Sequence
C 47	13	2.5	20	6	AR262248	AR262248 Sequence
C 48	13	2.5	20	6	AR359747	AR359747 Sequence
C 49	13	2.5	20	6	AX149139	AX149139 Sequence
C 50	13	2.5	20	6	AX281333	AX281333 Sequence
C 51	13	2.5	20	6	AX342562	AX342562 Sequence
C 52	13	2.5	20	6	AX347474	AX347474 Sequence
C 53	13	2.5	20	6	AX402789	AX402789 Sequence
C 54	13	2.5	21	6	AR296505	AR296505 Sequence
C 55	13	2.5	21	6	AR567769	AR567769 Sequence
C 56	13	2.5	22	6	AR068025	AR068025 Sequence
C 57	13	2.5	22	6	AR120228	AR120228 Sequence
C 58	13	2.5	22	6	AR179906	AR179906 Sequence
C 59	13	2.5	22	6	AR182279	AR182279 Sequence
C 60	13	2.5	22	6	AR371883	AR371883 Sequence
C 61	13	2.5	22	6	AX718077	AX718077 Sequence
C 62	13	2.5	22	6	BD017061	BD017061 Novel pol
C 63	13	2.5	22	6	BD088974	BD088974 A method
C 64	13	2.5	23	6	AX004025	AX004025 Sequence
C 65	13	2.5	24	6	AR069189	AR069189 Sequence
C 66	13	2.5	24	6	AR102700	AR102700 Sequence
C 67	13	2.5	24	6	I64407	I64407 Sequence 23
C 68	13	2.5	24	6	AR183228	AR183228 Sequence
C 69	13	2.5	24	6	AR228157	AR228157 Sequence
C 70	13	2.5	24	6	AR364575	AR364575 Sequence
C 71	13	2.5	24	6	AX289764	AX289764 Sequence
C 72	13	2.5	24	6	BD015755	BD015755 Estrogen
C 73	13	2.5	25	6	AR158396	AR158396 Sequence
C 74	13	2.5	25	6	AR158397	AR158397 Sequence
C 75	13	2.5	25	6	AR158398	AR158398 Sequence
C 76	13	2.5	25	6	AR158399	AR158399 Sequence
C 77	13	2.5	25	6	AR158400	AR158400 Sequence
C 78	13	2.5	25	6	AR158401	AR158401 Sequence
C 79	13	2.5	25	6	AR158402	AR158402 Sequence
C 80	13	2.5	25	6	AR158403	AR158403 Sequence
C 81	13	2.5	25	6	AR158404	AR158404 Sequence
C 82	13	2.5	25	6	AR158405	AR158405 Sequence
C 83	13	2.5	25	6	AR158406	AR158406 Sequence
C 84	13	2.5	25	6	AR158407	AR158407 Sequence
C 85	13	2.5	25	6	AR158408	AR158408 Sequence
C 86	13	2.5	25	6	CO864140	CO864140 Sequence
C 87	13	2.5	25	6	CO864141	CO864141 Sequence
C 88	13	2.5	25	6	CO864142	CO864142 Sequence
C 89	13	2.5	25	6	CO875206	CO875206 Sequence
C 90	13	2.5	25	6	AR435187	AR435187 Sequence
C 91	13	2.5	25	6	AR435188	AR435188 Sequence
C 92	13	2.5	25	6	AR435189	AR435189 Sequence

C 93 13 2.5 25 6 AR435190  
 C 94 13 2.5 25 6 AR435191  
 C 95 13 2.5 25 6 AR435192  
 C 96 13 2.5 25 6 AR435193  
 C 97 13 2.5 25 6 AR435194  
 C 98 13 2.5 25 6 AR435195  
 C 99 13 2.5 25 6 AR435196  
 C 100 13 2.5 25 6 AR435197

## ALIGNMENTS

RESULT 1  
 BD254454/c 17 bp DNA linear PAT 17-JUL-2003  
 LOCUS  
 DEFINITION Regulation of repressor genes using nucleic acid molecules.  
 ACCESSION BD254454  
 VERSION BD254454.1 GI:33064224  
 KEYWORDS JP 2002541795-A/2247.  
 SOURCE unidentitied  
 ORGANISM unclassified.

REFERENCE  
 AUTHORS Blact,L., Zwick,M., Pavco,P. and Mcswiggen,J.  
 TITLE Regulation of repressor genes using nucleic acid molecules  
 JOURNAL Patent: JP 2002541795-A 2247 10-DEC-2002;  
 RIBOZYME PHARMACEUTICALS INC

COMMENT  
 OS Eukaryote  
 PN JP 2002541795-A/2247  
 PD 10-DEC-2002  
 PF 11-APR-2000 JP 2000611654  
 PR 12-APR-1999 US 60/123390  
 PI LAWRENCE BLATT, MICHAEL ZWICK, PAMELA PAVCO, JAMES MCSWIGGEN PC  
 C12N15/09,A61K38/00,A61P43/00,A61P43/00,C12N5/10, PC  
 C12P21/02,  
 PC C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC  
 C12R1:91)  
 PC (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,  
 PC A61K37/02,  
 PC (C12N5/00,C12R1:91)  
 CC Regulation of repressor genes using nucleic acid molecules FH  
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 /db\_xref="taxon:32644"

## ORIGIN

Query Match 3.0%; Score 16; DB 6; Length 17;  
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 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 GGCTGCAGACGCTT 481  
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 Db 16 GGCTGCAGACGCTT 1

RESULT 2  
 CQ006442 50 bp DNA linear PAT 16-JAN-2004  
 LOCUS  
 DEFINITION Sequence 5082 from Patent WO0147944.  
 ACCESSION CQ006442  
 VERSION CQ006442.1 GI:41013074  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
 1  
 AUTHORS Shinkens,R.A. and Leach,M.  
 TITLE Nucleic acids containing single nucleotide polymorphisms and  
 methods of use thereof  
 JOURNAL Patent: WO 0147944-A 5082 05-JUL-2001;  
 Curgan Corporation (US)  
 FEATURES  
 source Location/Qualifiers  
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 misc\_feature 25..26  
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 Accession number C943972159"

## ORIGIN

Query Match 3.0%; Score 16; DB 6; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 2.6e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 311 GGCGCCAGAACCGA 326  
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 Db 27 GGCGCCAGAACCGA 42

RESULT 3  
 C0866809 28 bp DNA linear PAT 10-SEP-2004  
 LOCUS  
 DEFINITION Sequence 27 from Patent WO2004054601.  
 ACCESSION C0866809  
 VERSION C0866809.1 GI:51987754  
 KEYWORDS  
 SOURCE synthetic construct  
 ORGANISM synthetic construct  
 other sequences; artificial sequences.

REFERENCE  
 1  
 AUTHORS Weise,M., Eulenberger,K., Molitor,A., Steuernagel,A., Nguyen,T. and  
 Katterle,Y.  
 TITLE Fwd, ppc1, adk3, cg3860, cdk4, cg7134, eip75b involved in the  
 regulation of energy homeostasis  
 JOURNAL Patent: WO 2004054601-A 27 01-JUL-2004;  
 Develogen Aktiengesellschaft fuer entwicklungsbiologische Forschung  
 (DE)

FEATURES  
 source Location/Qualifiers  
 1..28  
 /organism="synthetic construct"  
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 3' (5/6-TAMRA)"

## ORIGIN

Query Match 2.8%; Score 15; DB 6; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 9.8e+03;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 471 CAGACAGCCTTGCCA 485  
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 Db 14 CAGACAGCCTTGCCA 28

RESULT 4  
 AR089810 41 bp DNA linear PAT 07-SEP-2000  
 LOCUS  
 DEFINITION Sequence 92 from patent US 5994075.  
 ACCESSION AR089810  
 VERSION AR089810.1 GI:10016565  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 REFERENCE 1 (bases 1 to 41)